rwhulb-a.rpr

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

January 13, 2005, 15:03:32; Search time 33.3983 Seconds (without alignments) 3321.665 Million cell updates/sec

Title: Perfect score: Sequence:

RWHUIB-A 5953 1 MALRVLLLTALTLCHGFNLD......FKRQYKDMMSEGGPPGAEPQ 1153

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	cell surf	leukocyte su:	cell surface glyco	surface	hocyte fu	integrin alpha-E	integrin alpha-1	integrin alpha 2 s	VLA-2 protein homo	integrin alpha-2 c	integrin algha-1	lymphocyte-Peyer's	integrin alpha-4 c		integrin alpha cha	alphaP integrin -	cell surface glyco	VLA-3 alpha subuni	integrin alpha-5 (integrin alpha-V c	integrin alpha-v c	tin recep	integrin alpha-6 c	alpha-3		alpha-6	alpha-5	
SUM	, CI	RWHU1B	S00551	RWHU1C	803308	156126	A53213	A45226	145914	S44142	A33998	A35854	A41131	806046	I58409	T31437	JC7294	A35761	I55534	844250	A36108	T10050	A27079	B36429	A40021	A38457	A41543	A27421	S16516
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di	Query Match	100.0	76.3	59.0	26.1	26.0	19.5	18.6	18.4	18.2	18.2	θ.	11.2	ö	10.6	ö	7.6	9.6	9.5	9.3	9.5	9.0	•	•	8.9	٠	8.8		8.7
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496.5	495.5	493.5	492	488	486	474.5	473	454.5	452	433.5	426.5	391	309	301.5	299
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
ranoll surface alvacantoin (D11) presureor (validated) - human
N:Alternate names: complement receptor type 3 alpha chain: leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C; Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
•
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)
D. Deference number. 231108. WIITD.88215032. DMID.2457584
A:Accession: Alline
A:MOJ ecule type: mRNA
A:Residues: 1-1153 <cor></cor>
A; Cross-references: UNIPROT: P11215; GB: J03925; NID: q187284; PIDN: AAAS9544.1; PID: q307148
A; Note: part of this sequence was confirmed by protein sequencing
R; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mc
A; KCTETENCE TUMBET: AZBSIS; MUID:88ZS/ZIS; FMID:24S4S3I
A;ACCESSION: AZSYLS
A)MOLECULE LYPE: UKM. A.MOLECULE LYPE: UKM.
A/KEBIQUES: 1-495/201-4905/ F /90/1115/ AKMIN> A/KEBIQUES: 1-495/201-4905/ F /90/1115/ AKMIN> A/KEBIQUES: 1-495/201-4905/ F /90/115/ AMINEMANA
A)-LIOBS-TERETERICES: GB:MILOW4%; GB:U02-U/V; GB:MILOO4%; GB:AVV441, NID:9100303; FIDN:AMA334: 3.MOTOS THE surthors translated the codon TDC for residie 1139 as Thr
Annues the durings transferred the Cocon into the latter as as an above the matrix and the confirmation is not the matrix and the confirmation is not the matrix and the ma
Dichallay C . Braanit M B
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A.Title: The promoter of the CD11b gene directs myeloid-specific and developmentally requ
A; Reference number: A41600, MUID: 92073318, PMID: 1683702
A;Accession: A41600
A; Molecule type: DNA
A; Residues: 1-9 <she></she>
A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R; Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
A,Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic
A; Reference number: A94193; MUID:88190151; PMID:2833753
A; Accession: A30892
A; Molecule type: mRNA
A) residues: 51/-1042 ARCS
A;Cross-references: GB:MI8044
K!HickEtelin, DJ.; Hickey, M.; OZOLS, J.; Baker, D.M.; Back, A.L.; Kotn, G.J. Dron Matl Anad Cri II to A of 257-251 1080
FIGURE MALLS ACRES OF THE STANDARD TO A STANDARD TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE STANDARD TO THE STANDA
A:Reference number: A32218: WIID:8909893: PMID:2563162
A; Accession: A32218
A; Molecule type: mRNA
A, Residues: 9-1153 <hic></hic>
A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir A;Reference number: S00551; MUID:88312584; PMID:3044779 A;Accession: S00551
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                                                   NTIASKPPRDHVFQVNNFEALKTIQNQLREKIPAIEGTQTGSSSSFEHEMSQEGFSAAIT
                                                                                                                                                                                                                                                                                                                                                                                            HYYEQIRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA
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                                                                                                                                                                    SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
                                                                                                                                                                                                                                                                               IGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP
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                                                                                                                                 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
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leukocyte surface glycoprotein Mac-1 alpha chain precursor - mou NyAlternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change C;Accession: S00551; I59078
EMBO J. 7, 1371-1378, 1988
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                                                                                A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in aduring evolution.
A;Reference number: A46526; MUID:93123748; FMID:8419480
A;Recession: A46526; MUID:93123748; FMID:94824821.1; PID:9263049
A;Residues: 1-499,501-1153 <PLE>
A;Residues: 1-499,501-1153 <PLE>
A;Residues: 1-499,501-1153 <PLE>
A;Rote: the last three bases of intron 13, CAG, are included in some but not all mature A;Note: sequence extracted from NGIB backbone (NCBIP:121963)
A;Note: sequence extracted from NGIB backbone (NCBIP:121963)
B;Cothin. Biophys. Acta 874, 368-371, 1966
A;Title: N terminal sequence of human leukocyte glycoprotein Mol: conservation across spacession: A26031
A;Molecule type: protein
A;Residues: 17-31 <PIE>
A;Molecule type: protein
A;Residues: 17-31 <PIE>
A;Residues: 17-31 <PIE>
A;Residues: 17-31 <PIE>
A;Residues: 17-31 <PIE>
A;Residues: 152567; MUID:92144986; PMID:1346576
A;Attle: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: 152567; MUID:92144986; PMID:1346576
A;Attle: Aranglated from CD4 FMD A A CASTILL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)CORRETE GLOSTICANI, CASA
A)CORRETE GLOSTICANI, CASA
A)ACORRETE GLOSTICANI, CASA
A)ACORRETE GLOSTICANI, CASA
A)AMAD POSITION: 16p11.2-16p11.2
A,NOTE: promoter contains a GATA motif and two Sp1 consensus binding sites
A,NOTE: promoter contains a GATA motif and two Sp1 consensus binding sites
A,NOTE: promoter contains a GATA motif and two Nillebrand factor type A repeat home
C,Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C,1-16/Domain: signal sequence #status predicted <SIG>
F,17-1108/Domain: extracellular #status predicted <EXT>
F,148-318/Domain: von Willebrand factor type A repeat homology <WAZ>
F,17-1108/Domain: von Willebrand factor type A repeat homology <WAZ>
F,530-538/Region: calcium/magnesium binding #status predicted
F,530-538/Region: calcium/magnesium binding #status predicted
F,1109-1134/Domain: transmembrane #status predicted <ITM>
F,1109-1134/Domain: intracellular #status predicted <ITM>
F,1109-1134/Domain: intracellular #status predicted <ITM>
F,186,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
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C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
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ut or this sequence was confirmed by protein sequencing J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.
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99.9%; Pred. No. 0;
ive 1; Mismatches
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A;Molecule type: DNA
A;Residues: 1-9 <RES>
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A; Molecule type: DNA
A; Residues: 1-1153 < PYP.
A; Residues: 1-1153 < PYP.
A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A; Note: the authors translated the codon CAC for residue 569 as Gln
R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 564-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep
A; Reference number: 159078
A; Reference number: 159078
A; Reference number: 159078
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 11-44 < RES>
A; Cross-references: GB:M14293; NID:g198993; PIDN:AA39484.1; PID:g554193
C; Genetics:
C; Genetics:
A; Gene: Mac-1
C; Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homc
C; Keywords: cell adhesion; glycoprotein predicted < SIG.
C; Superfamily: cell adhesion; glycoprotein Mac-1 alpha chain #status experimental
F; 116/Domain: von Willebrand factor type A repeat homology < VWA2>
F; 1106-1129/Domain: transmembrane #status predicted < TWM>
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76.3%; Score 4542; DB 2; Length 1
Best Local Similarity. 74.4%; Pred. No. 2e-303;
Matches 859; Conservative 142; Mismatches 151; Indels
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1019 1019 1139 VVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSV 1079 FTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYK 1139 840 839 XKPWFVKPAESSSSSGGGALKSTTWINHPIFPANSEVTFNVTFDVDSHASFGNKLLLK 899 959 LSITESPMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTPFPPLDLSYRKVSTLQNQRS QRSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLK ANVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVS NIGORSI.PISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAP 960 NLGQRSLPVSVVFWIPVQINNVTVWDHPQVIFSQNLSSACHTEQKSPPHSNFRDQLERTP PALLPGQESYVRSKTETKVEPYEVHNPVPLIVGSSIGGLVLLALITAGLYKLGFFKRQYK DMMSEGGPPGAEPQ 1153 DMMNEAAPQDAPPQ 1153

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Call surface glycoprotein CD11a precursor - human
NyAlternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C;Species: SerFeb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S03308; A47458; A4755; A48759; S36044
R;Larson, R.S.; Corbi, Al.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A;Title: Primary structure of the leukocyte function associated molecule-1 alpha subunit:
A;Reference number: S03308; MUID:89139587; PMID:2537322
A;Reference under: S03308; MUID:89139587; PMID:2537322
A;Rolccule type: mRNA
A;Residues: 1-1170 < LAR>
A;Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA687;
A;Note: part of this sequence was confirmed by protein sequencing
R;Cornwell, R.D.; Gollahon, K.A.; Hickerein, D.D.
A;Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pron
A;Reference number: A47458
A;Rolccule type: DNA
A;Reference extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
A;Rolccule type: DNA
A;Residues: 1-20 < COR>
A;Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
A;Title: Identification of cell-specific and developmentally regulated nuclear factors th
A;Reference number: A47565; MUID:93281759; PMID:8099450
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A;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A : C;Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface an F;1-25/Domain: signal sequence #status predicted <SIG>F;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status F;154-317/Domain: von Willebrand factor type A repeat homology <WA2>
                                                 ENNMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
                                                                                                                              RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                              SIAVCQRIQCDIPFEGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLL
                                                                                                                                                                                                                                                                                                                                                 PGQGAFVRSQTETKVEPFEVPNPLPL1VGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
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A;Residues: 1-20 <SHE>
A;Cross-references: GB:M95609
B;Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J; Biol. Chem. 268, 19305-19311, 1993
A;Title: Characterization of the CD11a (alphaL, LFA-lalpha)
A;Reference number: A48759; MUID:93374910; PMID:8103515
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Pred. No. 3.1e-98;
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34.3%;
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A;Gene: GDB:ITGAL; CD11A
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A; Residues: 1-20 <NUE>
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C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; Fi-19/Domain: signal sequence #status predicted <SIS> Fi-19/Domain: signal sequence #status predicted <SIS> Fi-20-1163/Product: cell surface glycoprotein Collc #status predicted <MAT> Fi-20-1107/Domain: extracellular #status predicted <EXIN> Fi-149-319/Domain: von Willebrand factor type A repeat homology <VWA4> Fi-149-313/Domain: transmembrane #status predicted <TWN> Fi-1103/Domain: intracellular #status predicted <INT> Fi-1134/Domain: intra
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OY 1040 IQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVE 1099 :	RESULT 5 IS6126 lymphocyte fuction-associated molecule-1-alpha - mouse C:Species: Mus musculus (house mouse) C:Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C:Accession: 156126 C:Accession: 156126 R;Kaufmann, Y: Tseng, E.; Springer, T.A. J. Immunol. 147, 369-374, 1991	A; Reference number: 156126; MUID:91268576; PMID:2051027 A; Reference number: 156126; MUID:91268576; PMID:2051027 A; Returus: pre-aliminary; translated from GB/EMBL/DDBJ A; Molecule type: mENA A; Residues: 1-1163 < RES> A; Residues: 1-1163 < RES> A; Residues: 1-1163 < RES> A; Residues: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786	A;Gene: LFA-1 C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol F;151-315/Domain: von Willebrand factor type A repeat homology <vwa1></vwa1>	Query Match 26.0%; Score 1546; DB 2; Length 1163; Best Local Similarity 34.1%; Pred. No. 1.5e-97; Matches 408; Conservative 217; Mismatches 464; Indels 106; Gaps 38;	OY 1 MALRVLLITALTLCHGFNLDTENAMTFQENA-RGFGQSVVQLQGSRVVVGAPQ 52	QY 53 EIVAANQRGSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQT 112	OY 113 CSENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEF 172	QY 173 VSTVMEQLKKSKTLFSLMQYSBERIHPTFKBF-QNNPNPRSLVKPITQLGGRTHTATGI 231	OY 232 RKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYV 284	OY 285 IGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFBALKTIQNOLREKKFAIEGTOTGSSS 344 : : : : :	OY 345 SFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAY 403	QY 404 LGXAAA-IILRNRVQSLVLGAPRYQHIGLVAMPRQNTGMWESNANVKGTQIGAYFGAS 460	OY 461 LCSVDVDSNGSTDLVLIGAPHYYEQTRCGQVSVCPLPRCQRARWQCDAVLYGEQGQPWGR 520	OY 521 FGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPR 580
Matches 409; Conservative 211; Mismatches 464; Indels 110; Gaps 38; Qy 6 LLLTALTLCHGFNLDTENAMTEQENARGEGGSVVQLGGSRVVVGAPQEI 54	QY 115 ENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMK 170	237 INYVATBVFREELGARPDATKVLIITDGEATDSGNIDAAKDIIRYIIGIGKH 291 FRSEKSROELNTIASKPPRDHVFQVNNFBALKTIQNOLREKXFAIEGTQTGSSSSFEHEM 290 FQTKESQETLHKFASKPASEFVKILDTFEKLKOLFTELQKKIYVIEGTSKQDLTSFNMEL	351	Qy 410 -IILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDV 466 :	OY 467 DSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAA 524	Qy 525 LTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYF 584 :	OY 585 GQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVXAIMEFNPREVARNVFECNDQVV 644	OY 645 -KGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQT 703	OY 704 QVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLÅPVL, 753	OY 754 AEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGSD 813 1 ::	OY 814 SYRIQVEFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPI 871	QY 872 PPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEFQLELPVKKAVY 927	OY 928 MVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFLVPVRLNQTVI 983	984 WDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFG 1039

64 PGPLHRCSLVQDEILCHPVEHVPIPKGRHRGVTVVRSHHGVLICIQVLVRRPH 116 111 QTCSENTYVKGLCFLFGSNLRQQPQ	240 NITNGARKNAPKILIVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQE 299 :: : :	471 TCSLAYVAĞAPQYKHIĞAYFELQKEĞREASFLPVLEĞEQMGSYFĞSELÇPVIDIMGĞS 528 472 TDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARMQCDAVLYGEQQQPMGREGAALTVLGDV 531	GKEAGEWRYCLHVOKSTRDRIREGOIOSVUTYDLALDSGRPHSRAVENETKNSTRROTOV
8 8 8 8 8 8	8 8 8 8 8 8	8 6 8 6 8 8	6 B 6 B 6 B 6 B 6 B 6 B 6
OY 581 LOYFGOSLSGGODLTMDGLVDLTVGAOGHVLLLRSOBVLRVKAIMEENPREVARNVEECN 640 1	810 DGE 805 SGE 869 HPI 860 SPI 860 SPI 928 MVV 928 MVV		RESULT 6 RABSULT 6 R

. q ₀	133	YTTGVCSDVSPDF-QLRTSFAPAVQTCP-SFIDVVVVCDESNSIYPWDAVKNFLEKFV 188
λ	178	BQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGI 231
οp	189	QGLDIGPTKTQMGLIQYANNPRVVFNLNTFKSKDEMIKATSQTFQYGGDLTNTFKA1 245
Vo	232	RKVVRELPNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPBADREGVIRVIGV 287
qq	246	QYARDTAYSTAAGGRPGATKVMVVTDGESH-DGSKLKAVIDQCNKDNILRFGIAVLGYL 304
& 8 &	305	-GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKXPAIEGTQTGSSSSF 346 :
λ̈́O	347	40
Db	364	: : :
ò	402	AYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGA 455
QQ	424	SYLGYSVASISTGNSVHFVAGAPRANYTGQIVLYSVNBNGNVTVIQSQRGDQIGS 478
λ̈σ	456	YFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLFRGQRARWQCDAVLYGE 513
QQ	479	YFGSVLCAVDVNKDTITDVLLVGAPMYMNDLKKEEGRVYLFTITKG-ILNWHQFLEGF 535
λ̈σ	514	OGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIA 573
Dp	536	NGLENARFGSAIAALSDINMDGFNDVIVGSPLENQNSGAVYIXNGHEGM-IRLRYSQKIL 594
δ	574	GSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPRE 631
qq	595	GSDRAFSSHLQYFGRSLDGYGDLNGDSITDVSVGAFGQVVQLMSQSIADVSVDASFTPKK 654
٥٨	632	VARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPH 687
qq	655	ITILINKNAEIKLKLCFSAKFRPTNQNNQVAIVYNITIDEDQFSSRVI 701
٥٧	688	SRAVENETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPL 743
Db	702	SRGLFKENNERCLQKTMIVSQAQRCSEYIIHIQEPSDIISPLNLCMNISLENPGT 756
٥⁄	744	SAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPR 799
Ωp	757	NPALEAYSETVKVFSIPFHKDCGDDGVCISDLVLNVQQLPATQQQPFIVSNQNK 810
٥٨	800	EFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLONQRSQRSWRLACESASST-EVSG 858
qq	811	RLTFSVQLKNKKESAYNTEIVVDFSENLFFASWSMPVDGTEVTCQ1AS 858
٥٨	859	ALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEFQL 918
qq	859	SOKSVICHVGYPALKSKQOVFFINFDFNLQ-NLQNQASISFRALSESQEENMADNSVNL 917
δ	919	>
ସ୍ପ	918	KLSLLYDAEIHIT-RSTNINFYEVSLDGNVSSVV-HSFEDIGPKFIFSIKVTTGSVPV 973
λά	696	SLVFLVPVRLNQTVIWDRPQVIFSENLSSTCHTKERLPSHS 1009
eg G	974	SMASVIIHIPQYTKDKNPLMYLTGVHTDQAGDISCEAEINPLKIGGTSSSV 1024
à	1010	DFLAE-LRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIV 1068
qq	1025	SFKSENFRHIKELNCRTASCSNIMCWLRDLOVKGEYFLNVSTRIWNGTFAASTFOTVOLT 1084
λα	1069	STAEL-LFNDSVFTLLPGQGAFVRSQTETKVEPFE-VPNPLPLIVGSSVGGLLL 1120
d d	1085	NPQIYVIEENT
ò	1121	LALITAALYKLGFFKRQYKDM 1141
qg ,	1135	LALVALLWKLGFFKRKYEKM 1155

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VIA-2 protein homolog - mouse
C;Species: Mus musculus (house mouse)
C;Becies: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44142
R;Bedlama, J.M.; Chan, B.M.; Unival, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latzers submitted to the EMBL Data Library, January 1994
A;Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not v
A;Reference number: S44142
A;Reference number: S44142
A;Reference repe: mRNA
A;Residues: 1-1178 <EDB-
A;Residues: 1-1178 <EDB-
A;Residues: 1-1178 <EDB-
A;Cross-references: UNIPROT: Q62469; EMBL: Z29987; NID: 9473098; PIDN: CAA82877.1; PID: 9473098; F;169-344/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                        44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 HTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 GV-----GDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AVLGYLNRNALDTKNLIKEIKAIASTPTERYFFNVADEAALLEKAGTLGEQIFSIEGTVQ 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|: ||: ||| | :: :| ||: ||: :| 367 G-GDNFQMEMAQVGFSADYAPQNDII.MLGAVGAFDWSGTLVQETSHKPVIFPKQAFDQVL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 ODRNHSSFLGYSVAAISTEDGVHFVAGAPRANYTGOIVLYSVNK---OGNVTVIOSHRGD 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 QIGSYPGSVLCSVDVDXDTITDVLLVGAPTYMNDLKKEEGKVYLFTITKGILNQHQ---F 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSSSFEHEMSQEGFSA--AITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDMN-DAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGT 451
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                                                                                                                                                                                                                                                                                                           Length 1178;
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                                                                                                                                                                                                                                                                                                      GPPENRMGDVYKCPVDLSTATCEKLNLQTSTSIPNVTEMKTNMSLGLILTRNMGTGGFLT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DADGFSSRVTSRGLFKENNERCLQKNMVVNQAQSCPEHIIYIQEPS---DVVNSLDLRVD 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             851
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                                                                                                                                                                                                                                                                               104
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCPLPRGQRAR
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                                                                                                                                                                                                                                                                                 54 IVAANQRGSLYQC--DYSTGSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLA
                                                                                                                                                                                                                                                                                                                                                                                         CGPLWAQQCGNOYYTTGVCSDISPDF-QLSASFSPATQPCPSL-IDVVVVCDESNSIYPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 GTVQG-GDNFQMEMSQVGFSADYSSQNDILMLGAVGAFGWSGTIVQKTSHGHLIFPKQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 -RVDSDMN-DAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 HQ---FLEGPEGIENTRFGSAIAALSDINMDGFNDVIVGSPLENQNSGAVYIYNGHQGT-
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                                                                                                                                                                                                       LRVLLLTALT -----LCHGFNLDTENAMTFQ-ENARGFGQSVVQL----QGSRVVVGAPQE
                                                                                                                             Length 1181;
                                                                                                                                                                  498; Indels 193;
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1133/Domain: extracellular #status predicted <EXT>
F;172-347/Domain: von Willebrand factor type A repeat homology
F;1134-1154/Domain: tracellular #status predicted <TWM>
F;1151-1181/Domain: intracellular #status predicted <CYT>
F;105,112,343,432,460,475,699,1057,1074,1081/Binding site: carb
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N;Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor al
C;Species: Homo sapiens (man)
C;Dacess: Homo sapiens (man)
C;Dacession: A33998, #sequence revision 18-Sep-1992 #text_change 09-Jul-2004
C;Accession: A33998, B56793; A53117
R;Takada, Y.; Hemler, M.E.
A;Tatle: The primary structure of the VLA-2/collagen receptor alpha(2)-subunit
A;Reference number: A33998; MUID:89308879; PMID:2545729
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   SRVTSRGVFRENSERFLOKKMMVVNEVQKCSEHHISIQKPS---DVVNPLDLRVDISLENP 762
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A;Map position: 5q11.1-5q11.2
C;Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein
                                                                                                                LVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESAS
                                                                                                                                                     ----ASFSMPVDGTE
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                                                                                                                                                                                                               NKADNSVSLTIPLLYDAELHLT-RSTNINFYEISSDENAPSVIK---SVEDIGPKFIFSL
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                                                               GTS-----PALEAYSETVKVFSIPPYKECGSDGICISDLILDVQQLPAIQTQSF----
                                                                                                                                                                                                                                                               NKTE--FQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR----
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A;Rebidues: 1-16,'V', 18-21 <ZUT>
A;Cross-references: GB:L24121; NID:g400342; PIDN:AAA16619.2; PID:g4583535
A;Note: authors translated the codon GTA for residue 17 as Leu
                                      PLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSI----
                                                                                                                                   1105 NPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDM 1141
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QY 402AYLGYAAAIILRNRVOSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFG 458 1	723 VTLDŠLRQIŠRŠFFSGTQERKIQRNITVRESECIRHSFYMLDK 724 EDPVSPIVLRINFSLVGTPLSAFGNIRPVIA-BDAQRLFTALFPFEKNGGNDNICQDDLSI 1	Db 923 SDSEEPLESLANDNEVNISIPVKYEVGLQFYSSASEHHISVAANETIPEFINSTEDIGN 980 QY 951 VMQHQYQVSNLGQRSLPISLVPLVPVRLNQTVIWDRP 987	SULT 12 1131 mphocyte-Pey Alternate na Species: Mus Date: 05-Jun Accession: A Cell Biol. Title: Cloni Reference m Accession: A
Db 962 EVTCQVAASQKSVACDVGYPALKREQQVTFTINPDFNLQ-NLQNQASLSFQALSESQEEN 920 Qy 911 TUKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR 964 Db 921 KADNLVNLKIPLLYDAEIHLTRSTNINFYEISSDGNVPSIVHSFEDVGPKFIFSLK 976 Qy 965SLPISLVFLV	F.; Carbonetto, or for laminin a 1; PID:g56494	Gaps 47; Gaps 47; 2PKARTG 77 COPTVHQ 111 CGPLYAY 136 DFRRMKE 171 FERMINE 171	192 FINDLLKRMDIGPKQTQVGIVQYGENVTHEFNIANKYSSTEEVLVAANKIGRQGGLQTMTA 251

S S	RESUL 15840	integ C;Spe C;Dat	R;Hib Oncog A;Tit	A; Ker A; Aco A:Sta	A; Res	K; Pall J. Ce. A; Tit. A; Ref	A; ACC A; Sta A; Mol A; Res	A; Cro C; Sup C; Key F;1-2	Que Bes Mat	P &	장 임	\$ 8	ζς Q	& <u>8</u>	& €	<i>8</i> €	ð	qu	ð í	යු
112 TCSENTYVKGLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKE 171 123 TCLEERDNOWLGVTLSROPGE147	FVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGI	RKVVRELFNITNGAR-KNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA	148 TYCGHRWKNIFYIKNENKLPTGGCYGV 174 291 FRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEM 350	175PPDLRTELSKRIAPCYQDXVKKFGENFAS 203	351 SQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDWNDAYLGYA 407	408AAIILRNRVQSLVLGAPRXQHIGLVAMFRQNTGWWESNANVKGTQIGAYFGASL 461 	462 CSVDVDSNGSTDLVLJGAPHYYEQTRGGQVSVCPLPRGQRARWQC-DAVLYGEQQPWGR 520	521 FGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVXLFHGTSGSGISPSHSQRIAGSKLSPR 580 :-	581 LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFE 638	639 CNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFN 693	694 ETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGN 748	749 LRPVLAEDAQR-LFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREF 801	802 NVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALK 861	862 STSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEFQLE 919	920 LPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-ISLVFL 973	974 VPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAV 1027	CORIOCDIPFFGIOEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFN	867 CALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKADPHCLNFLCNFGKMES 915	DSVFTLLPQQAFVRSQTETKVEPPEVPNP	916 GKEASVHIQLEGRPS-ILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVLLEGLH 974
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 Qy 1107LPLIVGSSVGGLLLALITAALYKLGFFKRQYKDWMSE 1144 : :
RESULT 14 158409 integrin alpha-9 chain precursor - human C;species: Homo sapiens (man) C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
ari, M.; Uchida, K.;
A;Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small A;Reference number: I58409; MUID:94119603; PMID:8290272 A;Accession: I58409
 A;Cross-references: UNIPROT:Q13797; GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g533327 R;Palmer, B.L.; Ruggy, C.; Ferrando, R.; Pytela, R.; Sheppard, D. J. Cell Biol. 123, 1289-1297, 1993
 A; Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partner A; Reference number: A49459; MUID:94064789; PMID:8245132 A; Accession: A49459
 A;Status: preliminary A;Molecule type: mRNA A;Residues: 30-1035 <pal></pal>
 A;Cross-references: GB:1124158 C;Superfamily: integrin alpha-4 chain C;Keywords: glycoprotein; metal binding; transmembrane protein F;1-27/Domain: signal sequence #status predicted <81G>
 Query Match 10.6%; Score 630; DB 2; Length 1035; Best Local Similarity 26.5%; Pred. No. 1.1e-34; Matches 237; Conservative 160; Mismatches 332; Indels 164; Gaps 40;
QY 347 EHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT-RVDSDMNDAYLG 405
 406 YAAAIILRNRVQSLVLGAPRYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASL
KGIGKVYIFRADRRSGTLIKIFQASGKKMGSYF
 Qy 462 CSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRF 521
 Qy 522 GAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRL 581 ::
 OY 582 QYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMBFNPREVARNVFEC 639
 640 NDQVVKGKBAGEVRV-CLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAV
 VTTCFSFHGKHVPEEIGLNYVLMADVAKKEKGQMPRVY
 OY 692 FNETKNSTRROTQVIGLTQTCETIKIQLPNCIEDPVSPIVLRINFSLVGTPLS 744
Qy 745 AFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCL 793 Dh 592 RippippirawkkgokraoknomvFFRNPSED-CAADLOLOGKIII.SSMDEKTIVI. 647
794 VVGGPREPNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQNQRSQRSWRLACESASS
Db 648 ALGAVKNISLNISISNLGDDAYDANVSFNVSRELFFINMWQKEBMGISCELLES 701

675	830 RKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNIT 883 :::::::::::::::::::::::::::::::::::		835 MTEEGVTCQLTQGKANPEGVKLEPSTKAKLSNSTTQVSGRKRREPEVAEALAQTDNVI 892 1022 NCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILF 1075	1076 NDSVPTLLPQQQAFVRSQTETKVEPFEVDNP	1109 -LIVGSSVGGLLLALITAALYKLGFFKRQYKDMMSEGGPP 1148	Search completed: January 13, 2005, 15:13:21 Job time : 44.3983 secs							
6 6 6 6 6 6	8 6 8 6	\$ 8 \$	8 & 8	& 8	& g	Sea Job							
	Qy 1005 LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFD 1055 Db	Qy 1101FEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMM 1142	1314937 integrin alpha chain SU2 - sea urchin (Lytechinus variegatus) C:Species: Lytechinus variegatus (variegated urchin) C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C:Accession: 131437, n.p.	Asherizier, T. J., "ACLAY, Data Library, May 1998 Ashescription: Alpha SU2, a sea urchin integrin which binds laminin. Askeference number: 221035	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1041 <hbr> A;Cross-references: UNIPROT:076378; EMBL:AF067658; NID:g3220240; FID:g3220241; PIDN:AACZ A;Experimental source: developmental stage embryo</hbr>	C;Function: A;Description: binds laminin C;Superfamily: integrin alpha-2b chain	Query Match 10.3%; Score 614.5; DB 2; Length 1041; Best Local Similarity 24.8%; Pred. No. 1.3e-33; Matches 236; Conservative 155; Mismatches 314; Indels 245; Gaps 41;	Qy 352 QEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLG 405	OY 406 YAAAIILRNRVQSLVLGAPRYQHI-GLVAMFRQNTGMWBSNANVKGTQLGAYFGÄSLC 462 : : :	OY 463 SVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQ 514 :: : : : : : : : : : : : : : : : : :	Qy 515GQPWGREGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGS 562	QY 563 GISPSHSQRIAGSKIS-PRLQYFQOSLSGGQDLTWDGLVDLTVGAQGHVLLLRSGPVL 619 : :	Qy 620 RVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDELREGQIQSV 674 : : : : : 1 1 Db 463 SLDATLNTEPIGINLENKTYE-LADGTWVTSFIAMT 497

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OM protein - protein search, using sw model

January 13, 2005, 15:04:07; Search time 241.379 Seconds (without alignments) 2748.409 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

RWHUIB-A 5953 1 MALRVLLITALTLCHGFNLD......FKRQYKDMMSEGGPPGAEPQ 1153

Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P11215 homo sapien	P05555 mus musculu	Q9ji30 rattus norv	Q28984 sus scrofa	P20702 homo sapien	homo	mus m	Bad21383 mus muscu	Q9qxh4 mus musculu		P61625 bos taurus	P20701 homo sapien	Q6tyb8 bos taurus	Aaq90015 bos tauru	P24063 mus musculu	Q9wtv4 mus musculu	Q9r200 mus musculu				Q8hzv0 bos taurus	088340 rattus norv	_	P38570 homo sapien	O88341 rattus norv	рошо	Q9ukx5 homo sapien	bos t	Q6p1c7 mus musculu	Aah65139 mus muscu	Q62469 mus musculu
SUMMARIES	ΩI	ITAM HUMAN	ITAM MOUSE	0 <u>E</u> 106Ö	Q28984	ITAX HUMAN	ITAD_HUMAN	Q6KAS4	BAD21383	ITAX_MOUSE	ITAD RAT	ITAL BOVIN	ITAL_HUMAN	Q6TYB8	AAQ90015	ITAL MOUSE	Q9WTV4	Q9R200	Q98TF1	Q98TF0	096нв1	OSHZV0	088340	ITAE MOUSE	ITAE HUMAN	088341	ITA1 HUMAN	ITAH HUMAN	ITA2_BOVIN	Q6P1C7	AAH65139	ITA2_MOUSE
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## ALIGNMENTS

Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00342; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
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GO; GG:0008305; C:integrin complex; TA
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PF01805; FG-GAP; 3.
Pfam; PF018057; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PDB; 1BHO; X-ray; 1/2=-
PDB; 1BHO; X-ray; 1/2=-
PDB; 1IDN; X-ray; 1/2=-
PDB; 1IDN; X-ray; @=140-331.
PDB; 1JIM; X-ray; @=143-334.
PDB; 1MIV; X-ray; @=143-337.
PDB; 1MY; X-ray; A=144-337.
PDB; 1MX5; X-ray; A=140-335.
PDB; 1MX5; X-ray; A=140-335.
PDB; 1MX5; X-ray; A=140-335.
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SMART; SM00327; VWA; 1.
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EMBL; M18044; AAA59491.1; -.
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PRINTS; PR00453; VWFADOMAIN.
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MEDLINE=98226734; PubMed=9560195;

A DOVAYG C., Springer T.A.;

BEDLINE=98226734; PubMed=9560195;

A OVAYG C., Springer T.A.;

Springer T.A.;

Springer T.A.;

Springer T.A.;

Subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. Us.A. 95:4870-4875(1998).

In Proc. Natl. Acad. Sci. Us.A. 95:4870-4875(1998).

The FUNCTION: Integrin alpha-M/beta-2 is implicated in various as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in G3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen gamma chain.

C -1 SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M associates with beta-2.

SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M associates with beta-2.

TISSUB SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                       MEDLINE=87076671; PubMed=3539202; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
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MEDLINE-95171458; PubMed-7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin (CR3 (CD11b/CD18).";
CR3 (CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE=5636571; PubMed=8747460;
MEDLINE=5636571; PubMed=8747460;
"To, Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE=98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzl., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Midner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
                                   SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318, PubMed=1683702;
Shelley C.S., Armout M.A.
"The promoter of the CDlib gene directs myeloid-specific and
                                                                                                                                                                               TISSUE=Blood;
MEDLINE=22144986; PubMed=1346576;
MEDLINE=2214086; PubMed=1346576;
"Characcerization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                            developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991)
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DD   960 LGQRSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1019	RESULT 2 ITAM MOUSE ID _ITAM MOUSE STANDARD; PRT; 1153 AA. AC P05555; Q8CA73; DT 01-NOV-1988 (Rel. 09, Created) DT 01-FEB-1991 (Rel. 17, Last sequence update) DT 05-UL-2004 (Rel. 44, Last annotation update)		RP SEQUENCE FROM N.A. (ISOPORM 1).  RX MEDLINE=88312584; PubMed=3044779;  RA Pytela R.;  RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology  RT with the integrin family and an additional domain related to von  RI Willebrand factor.;  RL EMBO J. 7:1371-1378(1988).	DUBNICE FROM N.A. (ISOFORM 2).  MAIN-C57BL/6J; TISSUB-Spinal cord;  MAIN-C57BL/6J; TISSUB-Spinal cord;  MAIN-C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;  MAIN-C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;  MAIN-C57BL/6BL/6BL/6BL/6BL/6BL/6BL/6BL/6BL/6BL/6	RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Dallas E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gasterland T., Gariboldi M., Giasi C., Godzik A., Gough J., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D., RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.,	RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M., RA Ravasi T., Reed J.C., Reed J.C., Semple C.A., Setou M., Shimada K., RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., RA Verardo R., Wagner L., Wahleetedt C., Wang Y., Watanabe Y., Walls C., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., RA Hara A., Hashizume W., Imctani K., Ishini Y., Itoh M., Kagawa I., RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., RA Birney B., Hayashizaki Y., RA Birney B., Hayashizaki Y., RT Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-langth cDNAs."; Nature 420:563-573 (2002).	RN [3] RP SEQUENCE OF 11-45 FROM N.A. RC STRAIN=BALB/c; TISSUE=Spleen;
PT SIGNAL   1   16	121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 180	ROEL       ROEL AAIT	OSEV OSEV IGAP	HYYEOTRGGOVSVCPLPRGORARWOCDAVLYGEOGDWGRFGALTVLGDVNGDYLTDVA HYYEOTRGGOVSVCPLPRGORARWOCDAVLYGEOGDPWGRFGALTVLGDVNGDYLTDVA HYYEOTRGGOVSVCPLPRAFWQCDAVLYGEOGOPWGRFGAALTVLGDVNGDYLTDVA TGAPGEEDNRGAVYLFHGTGSGISPSHSQRIAGSKLSPRLQYFGOSLGGODTTWDGLV TGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLGGODTTWDGLV TGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGOSLGGODTTWDGLV	601 DLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK 660	721 NCIEDPVSPIVLRIAFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD 780	Qy         841 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKA 900           Db         840 QRSWRLACESASSTEVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKA 899           Qy         901 NVTSENNWPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960           Db         900 NVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 959	961 LGGRSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020

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**Springer T.A., Teplow D.B., Dreyer W.J.; **

**Springer T.A., Teplow D.B., Dreyer W.J.; **

**Isequence homology of the LRA-1 and Mac-1 leukocyte adhesion and unexpected relation to leukocyte interferon."; **

**Isequence homology of the LRA-1 and Mac-1 leukocyte interferon."; **

**Isequence homology of the LRA-1 and Mac-1 leukocyte interferon."; **

**Isequence homology of the LRA-1 and Mac-1 leukocyte interferon."; **

**Isequence homology of the LRA-1 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes adhesive interactions of monocytes, macrophages and granulocytes and mast cell development and in immune complexemediated for the third complement and in immune complexemediated complexement and in immune complexemediated glomerulonephritis. Mice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophila accumulation, in response to a impaired degranulation and phagocytosis, events that constrains apparently accelerate apoptosis in neutrophils. These mice develop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-1- SIMILARITY: Belongs to the integrin alpha chain family.
-1- SIMILARITY: Contains 7 FG-GAP repeats.
-1- SIMILARITY: Contains 1 VWFA domain.
                  Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental confirmation available; IISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X07640; CAA30479.1; --
EMBL; AK039444; BAC30350.1; --
EMBL; AL4293; AAA39484.1; --
EMBL; ML4293; AAA39484.1; --
EMBL; ML4293; AAA39484.1; --
EMBL; ML4293; AAA39484.1; --
HSSP; P11215; 1BHQ.
MAD; MGT: 96607; Itgam.
GO; GO:0008997; C:exernal side of plasma membrane; IDA.
GO; GO:0009897; C:exernal side of plasma membrane; IDA.
GO; GO:0009897; P:cellular extravasation; IMP.
GO; GO:003593; P:neutrophil chemotaxis; IMP.
InterPro; IPR0020413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P05555-2; Sequence=VSP_010473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
IsoId=P05555-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMI, PPO1839; FG-GAP; M. P. PERMI, PPO1839; FG-GAP; M. PERMI, PPO1092; INTEGRINA. PRINTS; PRO1485; VWFADOMAIN. PRINTS; PRO0453; VWFADOMAIN. PROSTTE; SMO0191; VWFA, 1. PROSITE; PSO0242; INTEGRINALIS, PROSITE; PSO0242; INTEGRINALIS, 1.
MEDLINE=86287312; PubMed=2942940;
                                                                                                                                      SEQUENCE OF 17-28.
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GSLYQCDYSTGSCEPIRLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALRVLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR
PROSITE; PS50234; VWPA; 1.
Alternative splicing; Calcium; Cell adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
Signal; Transmembrane.
1 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1153 AA; 127480 MW; 178DB988AECB0343 CRC64;
                                                                                            Integrin alpha-M.
Extracellular (Potential)
                                                                                                                                                     Cytoplasmic (Potential)
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V -> G (in Ref. 2)
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GFFKR motif.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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FG-GAP 7.
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           Pathallah D.M. Sr., Zerria K. Jr.;

Rathallah D.M. Sr., Zerria K. Jr.;

I. Submitted (Max-2000) to the Embideance protein (By similarity).

Rathal Ap268331 AAF81280.1;

Rathal Ap268331 AAF81280.1;

Rathal Ap268331 AAF81280.1;

Rathal Ap268331; Integrin complex; IEA.

Roj GO:0007229; Pintegrin—alpha.

Rathal PP00032; VWP.A.

Rathal PP00032; VWP.A.

Rathal PP00032; VWA.1.

RATHALS SM00131; Int. alpha; J.

RAKRT; SM00131; Int. alpha; J.

ROSITE; PS00242; INTEGRIN ALPHA; I.

ROSITE; PS00242; INTEGRIN ALPHA; I.

ROSITE; PS00234; VWFA; I.

ROSITE; ROSIO33; VWFA; I.

ROSITE; ROSIO34; VWFA; I.
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                                                                                                          SNGPLLGSVGSFDWAGGAFLYTSKDKVTFINTTRVDSDMNDAYLGYASAVILRNRVQSLV
                                                                                                                                                                         LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP
                                                                                                                                                                                             IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLK
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                        SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alba subunit.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                    134 PQKFPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYS
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  64.3%; Score 3826.5; DB 2; Length
79.8%; Pred. No. 4.1e-243;
ive 78; Mismatches 107; Indels
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

- I- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

- I- SIMILARITY: Belongs to the integrin alpha chain family.

EMBL; U40072; AAB16869.1; -- integrin alpha chain family.

EMBL; U40072; AAB16869.1; -- integrin alpha chain family.

R GO; GO:0001160; P:cell-matrix adhasion; IEA.

InterPro; IPR00413; Integrin_alpha.

R InterPro; IPR002035; VWPA.

R PRINTS; PR00453; VWPA.

R PRINTS; PR00453; VWPADOMAIN.

SMART; SM00191; Int_alpha; 4.

R SMART; SM00191; Int_alpha; 4.
                                                                                NCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD
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Sus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae,
NCBI_TaxID=9823;
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Last annotation update)
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01-FEB-1997 (TEMBLIEL 02,
01-JUN-2003 (TEMBLIEL 24,
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                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
                          WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdllc.htm".
       DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GlcNAc.
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By similarity.
N-linked (GlcN
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EMBL; M29165; -; NOT ANNOTATED CDS.
EMBL; M29482; AAA51620.1; ALT SEQ.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29486; AAA51620.1; JOINED.
EMBL; M3948; AAA51620.1; JOINED.
EMBL; M39584; AAA51620.1; JOINED.
EMBL; M39584; AAA51620.1; JOINED.
EMBL; M39584; AAA51620.1; JOINED.
EMBL; M30584; AAA51620.1; JOINED.
EMBL; M30584; AAA51620.1; JOINED.
EMBL; M30584; AAA51620.1; JOINED.
EMBL; M30584; AAA51620.1; JOINED.
EMBL; M29685; JAMP, AAA51620.1; JAMP, AAA51
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FG-GAP
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       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Sheafer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Britchenko L., Marusiaa K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J., Usdin T.B., Tonahlyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tonahlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Racherds S., Worley W.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. M., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield S., S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Brown R. M., Roderson M., Marra M.A.,
Schentzch A., Schain J.E., Jones S.J.M., Marra M.A.,
Schenzton and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87167596; PubMed=3549901;
WEDLINE=87167596; PubMed=3549901;
MITHER LO.1, Wiebbe M., Springer T.A.;
MITHER LO.2, Wiebbe M., Springer T.A.;
And p150,95 leukocyte adhesion proteins.";
T and p150,95 leukocyte adhesion proteins.";
T Immunol 118:1381-2383(1987).
C Immunol 118:1381-2383(1987).
C Interaction during inflammatory responses. It is especially interaction during inflammatory responses. It is especially imporocyte adhesion and chemotaxis.
C Important in monocyte adhesion and chemotaxis.
C SUBCELLULAR LOCATION: Type I membrane protein.
C INSURE SPECIFICITY: Predominantly expressed in monocytes and
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DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=8816665; PubMed=3327687; Corbi A.L., MILLE.L.J., O'Connor K., Larson R.S., Springer T.A.; Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; CDMA cloning and complete primary structure of the alpha subunit of leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
01-FEB-1991 (Rel. 17, Created)
05-JUD-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu MS).
Name=ITGAX; Synonyme=CD11C;
Homo sapiens (Human).
                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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                          426 RYQHTGKAVIFTQVSRQWRMKAEVTGTQ1GSYFGASLCSVDVDTDGSTDLVLIGAPHYYE
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Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Local Similarity 61.3*; Pred, No. 4.3e-222;
les 700; Conservative 139; Mismatches 296; Indels 6
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                                T -> S (in Ref. 4).
T -> A (in Ref. 4).
G -> A (in Ref. 4).
G -> A (in Ref. 2).
E -> K (in Ref. 2).
D -> L (in Ref. 4).
I -> V (in Ref. 4).
SEK -> TPHYPQDNV (in Ref. 4).
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                                                                                                                                                                                                      SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE=96257236; PubMed=8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human beta 2-incegrin alpha subunit."; Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99059842; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                                           Noti J.D., Johnson A.K., Dillon J.D.; "Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Spl and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99370002; PubMed=10438935; Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Garaygon M.H., Bochner B.S., Gallatin W.M., Staunton D.E.; "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1."; or Interface between I domain and VCAM-1."; Interface Detween I domain and VCAM-1."; Interface Det
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6G; GO:0008305; C:integrin complex; TAS.
6O; GO:0016337; P:cell-cell adhesion; NAS.
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1 U40274; AAB60634.1; -...
1 U40275; AAB60635.1; -...
1 U40276; AAB60636.1; -...
1 U40277; AAB60638.1; -...
1 U40279; AAB60638.1; -...
                                                                          SEQUENCE OF 1-235 FROM N.A.
MEDLINE=20187620; PubMed=10722744;
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HSSP; P11215; 1BHQ.
Genew; HGNC:6146; ITGAD.
                                       Immunity 3:683-690(1995)
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INTERACTION WITH VCAMI
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R GO; GO:0007160; P:cell-matrix adhesion; NAS.
R GO; GO:000695; P:immune response; NAS.
R InterPro; IPR000413; Integrin_alpha.
R InterPro; IPR000413; Integrin_alpha.
R Pfam; PF00183; FG-GAP; 3.
R Pfam; PF00185; Integrin_alpha; 1.
R PRIMTS; PR00185; INTEGRINA.
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R PROSITE; PS034; VWFA; 1.
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-: SUMILARITY: Belongs to the integrin alpha chain family.

-: SIMILARITY: Belongs to the integrin alpha chain family.

REBL; AKISII33; BAD21383.1; -.

REBL; AKISII33; BAD21383.1; -.

RICEPTO; IPR000413; Integrin alpha.

RICEPTO; IPR002055; VWF A.

REPTO; PF00957; Integrin alpha; 1.

REPTO; PF00957; Integrin alpha; 1.
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Sciurognathi; Muridae; Murinae; Mus.
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PRINTS; PRO1453; VWFADOMAIN.
SMART; SMO191; Int_alpha; 5.
SMART; SMO0327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
PROSITE; PS50234; VWPA; 1.

CELL adhesion; Integrin; Transmembrane.
NON_TER.
                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
protein (Fragment)
                       Name=mFLJ00114;
Mus musculus (Mouse)
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MAS musculus (Mouse).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
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                                                                                                     CDYSTGSCEPIRLOVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFL
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                                                 LLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQ
                                                                                                                                                       FGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKT
                                                                                                                                                                                                          LFSLMOYSEEFRIHFTFKEFONNPNPRSLVKP1TOLLGRTHTATG1RKVVRELFN1TNGA
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                        Indels
          Pred. No. 4.4e-212;
; Mismatches 307;
57.2%;
                         Conservative
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Best Local 9
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                                                    1160
                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of genes selectively expressed by dendritic cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
I Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
I recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis (By similarity).

-!- SUBLNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2 (By similarity).

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-!- DOMAIN: The integrin 1-domain (insert) is a VWFA domain. Integrins with 1-domains do not undergo protease cleavage.

-!- SIMILARITY: Contains 7 FG-GAPP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
1041 HMQKSPVLDCSIADCLHLRCDIPSLGILDELYFILKGNLSFGWISQTLQKKVLLLSEAEI 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R HSSP; P20702; 1N3Y.

R MGD; MGI:96609; Itgax.
GO; GO00999; C:extranal side of plasma membrane; IDA.
GO; GO00999; C:extranal side of plasma membrane; IDA.
GO; GO00999; C:extranal side of plasma membrane; IDA.
R InterPro; IPR000413; Integrin_alpha.
R Pfam; PF00189; FR0-186; Integrin_alpha; 1.
R Pfam; PF00092; VWA; 1.
R PRINTS; PR01915; INTEGRINA.
R PRINTS; PR00191; Int alpha; 1.
R SWART; SM00191; Int alpha; 1.
R SWART; SM00191; Int alpha; 1.
R PROSITE; PS0024; INTEGRIN ALPHA; 1.
R PROSITE; PS0234; VWFA; 1.
R PROSITE; PS0234; VWFA; 1.
                                       1074 LENDSVFTLLPGQGAFVRSQTETKVBPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGF
                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
Name=Itgax;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.
Tsuchiya H.;
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
Integrin alpha-X.
Extracellular (Potential).
                                                                                                                                                                        PRT; 1169 AA
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SIGNAL 1 19 E
CHAIN 20 1169 E
DOMAIN 20 1116 E
                                                                           FKROYKDMMSE 1144
                                                                                                        FKRQYKEMLEE 1171
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                             musculus (Mouse)
                                                                                                                                                                       ITAX MOUSE
Q9QXH4;
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ITAX MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 RXNAFKILVVITDGEKFGDPLGYBDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 MPSHEYVFSVENFDALKDIENQLKEKIFAIEGTETPSSSTFELEMSQEGFSAVFTPDGFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 LGAVGSFSWSGGAFLYPSNWRPTFINMSQENEDMRDAYLGYSTALAFWKGVHSLILGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 EEENRGAVYIFHGASRODIAPSPSORISASQIPSRIQYFGQSLSGGODLTRDGLVDLAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVOSLVLGAPR
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                                                                                                                                                                                                                                                                                                                                                                                                       (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%; Score 3349.5; DB 1; Length 1169; llarity 57.0%; Pred. No. 1.7e-211; Conservative 169; Mismatches 307; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
                                                                                                                                                                                                                                                                                                                                                                         (Potential)
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              Cytoplasmic (Potential). FG-GAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GlcNAc. .)
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                                                                                                                                                                                                                         GFFKR motif.
By similarity.
No similarity.
By similarity.
By similarity.
No linked (GICNAC...
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                                    FG-GAP 1.
FG-GAP 2.
                                                                                                                    FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential
                                                                                                                                                                                          Potential Potential
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N-linked
Potential
                                                                                   FG-GAP 3.
FG-GAP 4.
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(GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
N-linked (GlCM.
SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
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GFFKR mot
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FG-GAP 2.
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FG-GAP 4
FG-GAP 5
FG-GAP 5
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                                                                                                                                                   EMBL; AF021334; AAF21241.1; -.
HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                Repeat; Signal; Transmembrane SIGNAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
711
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1161 AA;
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          PVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITF
                                                                                                                                         SFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQ-----
                                                                                                                                                                                                 GPPDLKTLVVGSDLELNVDVTVSNDGEDSYGTTVTLFYPVGLSFRRVAEGQVFLRKKEDQ
                                                                                                                                                                                                                                       --NQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGN
                                                                                                                                                                                                                                                       LREGGIOSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TTAD_RAT | STANDARD; | PRT; | 1161 AA. | Q9QYE7; | 05-UUL-2004 (Rel. 44, Created) | O5-UUL-2004 (Rel. 44, Last sequence update) | 05-UUL-2004 (Rel. 44, Last annotation update) | O5-UUL-2004 (Rel. 44, Last annotation upda
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002035; VWF.A.
Pfam; PF01039; FG-GAP; 3.
Pfam; PF00092; VWA; 1.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
SWART; SM00191; Int.alpha; 5.
SWART; SM00191; Int.alpha; 5.
SWART; SM00191; VWA; 1.
PROSITE; PS00242; VWRA; 1.
PROSITE; PS50244; VWRA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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Matches 662; Conservative 159; Mismatches 306; Indels
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Gene 325:97-101(2004).

-1- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothalial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes (By similarity).

-1- SUBMIT: Heterodimer of an alpha and a beta subunit. Alpha-L associates with beta-2 (By similarity).

-1- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

-1- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        05-UUL-2004 (Rel. 44, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-IA) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                      SEQUENCE FROM N.A.
PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;
Fett T., Zecchinon L., Baise E., Desmecht D.;
"The bovine (Bos taurus) CD11a-encoding cDNA: molecular cloning, characterisation and comparison with the human and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integrin alpha-L.
Extracellular (Potential)
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FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
FG-GAP 7.
Potential.
Potential.
GFFKR motif.
1165
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FG-GAP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
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                             Created)
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Repeat, Signal; Transmembrane
SIGNAL 1 23
STANDARD;
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1084
1105
1165
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324
3324
3397
452
572
627
627
627
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535
78
                          05-JUL-2004 (Rel. 44,
                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                               (CD11a).
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24
1085
1106
                                                                                                                                                                                                                                                                             glycoproteins.
Gene 325:97-10
                                                                                            chain) (CD11
Name=ITGAL;
BOVIN
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DISULFID
DISULFID
                                                                                                                                                                  Bovinae;
 ITAL BC
P61625;
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PQVTFS-ENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFN 1045
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                                     821
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P20701; 043746;
01-FEB1991 (Rel. 17, Created)
01-FEB1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
11tegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
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                                                                                                                                                                                                                  DVDSKASLGNKLLLKANVTS-----ENNMPRTNKTBFQLELPVKYAVYMVTSHGVS
                                                                                                                                                                                                                                                                                                                                         TKYLNFTASENTSRVMQHQYQV----SNLGQRSLPISLVFLVPVRLNQTVI----WD---R
                                                                                                                                                                                                                                                                                                                                                                            PLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM------SEGGPPGAEPQ
      SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDINE=89139587; PubMed=2237322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
"Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                QELSFRKVEIL---KPHSHVPVGCEELPEEAVVHS-RALSCNVSSPIFGEDSMVDIQVMF
                                                                                                                                                                                                                                                        LDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITF
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"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha
beta 2) integrin.";
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Catarrhini, Hominidae, Homo.
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Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Euftus B.J., Kim U.-J., Sneddon V.P., Kanush F., Brandon R.,
Euhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.Y., Kang H.-L., Mitchell S.,
Eichler B.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA seqn
denomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 153-335, AND
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MEDLINE=96398682; PubMed=8805579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
MEDLINE=96036067; PubMed=7479767;
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J. Cell Biol. 108:703-712(1989)
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=ITGAL; Synonyms=CD11A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVR 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRN 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQ 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 EVFRPDLGARPDATKVLIIITDGBATD----EHNIDAA--KDIIRYIIGIGKOPKTKBS
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                                                                                                                       (Potential).
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417; Conservative
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the CD11a/CD18 integrin.";

Structure 4:931-942(1996).

Structure 4:931-942(1996).

KAPA CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.

MEDLINE-99425288; PubMed=10493852;

A Cottens S., Weitz-Schmidt G., Hommel U.;

Cottens I domain.";

T Structural basis for LFA-1 inhibition upon lovastatin binding to the Cottens Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes.

C-1- SUBUNIT. Heterodiner of an alpha and a beta subunit. Alpha-L
                                                                                                                                                                                                                                                                                                                                                              Name=2,
Note=No experimental confirmation available;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
TISSUB SPECIFICITY: Leukcoytes.
DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1185; VMFADOMAIN.
PRINTS; PRO1185; VWFADOMAIN.
SWART; SMO0191; Int_alpha; 5.
SWART; SMO0192; Int_alpha; 5.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VMFA; 1.
3D-structure; Alternative splicing; Calcium; Cell adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Magnesium;
Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                         associates with beta-2.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=P20701-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 153370; -...
GO, GO:0008305; C:integrin complex; TAS.
GO; GO:0006928; P:cell mctility; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PP01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00392; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1CQP; X-ray; A/B=153-334.
PDB; 1DQQ; NNR; A=149-336.
PDB; 1LPA; X-ray; A/B=153-31.
PDB; 1MAN; X-ray; A=153-31.
PDB; 1MQB; X-ray; B/D=155-331.
PDB; 1MQB; X-ray; B/D=155-330.
PDB; 1MQB; X-ray; A=152-330.
PDB; 1ZON; X-ray; A=152-336.
PDB; 1ZON; X-ray; A/B=150-336.
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EMBL; AC002310; AAC31672.1; -.
PIR; S03308; S03308.
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Q -> QGYHGLVEMQTSKQILCRPAGDAEHTVGAQGGELPC
PWGVSEAFRDNIRAGPCR (in isoform 2).
                                                                                                                                                                                                                          (Potential).
(Potential).
(Potential).
(Potential).
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Pred. No. 1.6e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128819 MW; 39A7AF92EF286FC0 CRC64;
Integrin alpha-L.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                         R -> W (in Ref. 1 and 2).
Y -> I (in Ref. 2).
                  Potential.
Cytoplasmic (Potential).
FG-GAP 1.
                                                                                                                                                                                                                                                                                                              (GlcNAc. .)
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N-linked (GlcN.
                                                                                                                                          GFFKR motif
                                                                                                                      Potential
Potential
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                                               FG-GAP 2
                                                               FG-GAP 3
FG-GAP 4
FG-GAP 5
                                                                                            FG-GAP
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Best Local Similarity ' 34.3%;
                                                                                                              476
538
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1170 AA;
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IQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVE 1099
                                   63 GNSMGNLYQCQPETGDCLPVTLS--SNYTSKYLGMTLATDPTSDNLLACDPGLSRTCDQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IYLSGLCYLIHENLRGPVLQGHPGYQECIKGNVDLVFLFDGSMSLQQDEFEKIVDFMKDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 AAITSNGPLLSTVGSYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 TYVKGLCFLFGSNLROQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBLINTIASKPPRDHVFQVNNFBALKTIQNQLREKXFALEGTQTGSSSSFEHEMSQEGFS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVR
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                                                                                                                                                                                                                                                                                                                                                                   Dilegen T., Thumbikat P., Kannan M.S., Maheswaran S.K.;

Submitted (SEP-2003) to the EMBL/Genbank/DDBJ databases.

-1- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-1- SIMILARITY: Belongs to the integrin alpha chain family.

R EMBL; AY382558; AAQ90015.1; -.

R InterPro; IPR000413; Integrin_alpha.

R Pfam; PF01839; FG-GAP; I.

R Pfam; PF01839; FG-GAP; I.

R Pfam; PF00185; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR0191; Int alpha; 5.
                                                                                           1083 VVYEKQMLYLYVLSGIGGLLLLLIFIVLYKVGFFKRNLKEKMEAGRGVPNGIP 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                          PFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEG-GPPGAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.2%; Score 1557; DB 2; I
larity 34.2%; Pred. No. 2.5e-93;
Conservative 203; Mismatches 478;
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PROSITE; PS50234; VWFA; 1.
Call adhesion; Integrin; Transmembrane
SEQUENCE 1166 AA; 128723 WW; 7B8DB;
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                                                                                                                                                                               PRT;
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411; Conserv
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                               ENTYVKGLCFLFGSNLR----QQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMK 170
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QNTYLSGLCYLFRQNLQGPMLQGRPGFQECIKG---NVDLVFLFDGSMSLQPDEFQKIL 176
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                                                                                                                                                                                                                          IRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDA
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
Bos taurus (Bovine).
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                     Query Match 26.2%; Score 1557; DB 2; Length 11 Best Local Similarity 34.2%; Pred. No. 2.5e-93; Matches 411; Conservative 203; Mismatches 478; Indels
to the EMBL/GenBank/DDBJ databases
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128723 MW; 7B8D8AFBA896C9DF
            EMBL; AY382558; AAQ90015.1; SEQUENCE 1166 AA; 128723
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                                                                                                                                                                                                               1028 VQVNGMVELRGTIKAS-SMLSLCSSLAISFNSSKHFHLHGRNASM-AQVVMKVDLVYEKE 1085
                                                                                                                                                                                                                                                                                                               MLYLYVLSGIGGLILFLFIFIALYKVGFFKRNLKEKMEANVDASSEIPGEDAGQPELEKE 1145
                                                                             POVTPS-ENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFN 1045
                                                                                                                                                                                  1046 ATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPN 1105
                                                                                                                                                                                                                                                                                  1106 PLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM------SEGGPPGAEPQ 1153
                                                                                                                             PPVNCSPRNLESPSDEAB----ROGIL 1027
TLYISFTPKSPRIHHVKHIYQVRIQPSNYDNMP-PLBALVRVPRVHSEGLITHKWSIQME 990
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SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
associates with beta-2.
SUBCELULIAR LOCATION: Type I membrane protein.

TISSUE SPECIFICIATY: Leukocytes.
DOMAIN: The integrin I domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 4), Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91268576; PubMed=2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit and its expression in COS cells.";
J. Immunol. 147:369-374(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1163 AA
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PIR; I56126; I56126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Itgal; Synonyms=Lfa-1;
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HSSP; P20701; 1DGQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 VSTVMEQLKKSKTLFSLMQYSBEFRIHFTFKEF-QNNPNPRSLVKPITQLLGRTHTATGI
                                                                                                                                   PROSITE; PS00242; WFFGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
SIGNAL 24 1163 Integrin alpha-L.
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Extracellular (Potential)
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GFFKR motif
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N-linked
N-linked
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfan; PF01839; PG-GAP; 2.
Pfan; PF001839; Integrin_alpha; 1.
Pfan; PF00092; VWA; 1.
PRINTS; PR001185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SNART; SM00191; Int alpha; 5.
SWART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
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FG-GAP 2
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Search completed: January 13, 2005, 15:18:42 Job time : 249.379 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein January 13, 2005, 14:59:41; Search time 215.571 Seconds (without alignments) 1918.696 Million cell updates/sec Run on:

RWHU1B-A

1 MALRVLLLTALTLCHGFNLD......FKRQYKDMMSEGGPPGAEPQ 1153 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26 3452 58.0 1161 5 ABG61468 27 3436.5 57.7 1161 2 AAW623064 29 3436.5 57.7 1161 2 AAW623064 30 3436.5 57.7 1161 2 AAW72343 31 3436.5 57.7 1161 2 AAW72343 32 3436.5 57.7 1161 3 AAB07376 33 3261 54.8 1161 2 AAW623061 34 3261 54.8 1161 2 AAW623061 35 3261 54.8 1161 2 AAW623061 36 3261 54.8 1161 2 AAW723361 37 3261 54.8 1161 2 AAW723361 38 3261 54.8 1161 2 AAW723361 39 3261 54.8 1161 2 AAW723361 30 3257 54.6 1161 2 AAW73062 41 3250.5 54.6 1161 2 AAW73062 43 3248.5 54.6 1161 2 AAW73062 44 3248.5 54.6 1161 2 AAW72824 45 3248.5 54.6 1161 2 AAW72824 46 3248.5 54.6 1161 2 AAW72824	<b>AAAA</b>	Aaw65103 Mouse bet Aaw72836 Mouse alp Aab07373 Mouse alp Aab07373 Mouse alp Abg61482 Mouse Bet Aar78168 Mouse alp Aar78169 Rat alpha Aaw23062 Rat alpha Aaw72824 Rat alpha Aaw72824 Rat alpha
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	243 333 343 343 343 343 343 343 343 343	44444444444444444444444444444444444444

## ALIGNMENTS

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis. Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA (first entry) 28-SEP-1998 AAW65090; RESULT 1 AAW65090 

Homo sapiens

US5728533-A. 17-MAR-1998. 95US-00485618 07-JUN-1995; 23-DEC-1993;

93US-00173497. 94US-00286889. 94US-00362652. 05-AUG-1994; 21-DEC-1994;

(ICOS-) ICOS CORP.

Van Der Vieren M, Gallatin WM;

WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit alpha (AAA60014 and AAB07359). The present sequence has approximately 604 identity to the protein sequence of alpha d. The Alpha den and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatold arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha_d monoclonal antibodies may be used in the
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                             TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKD
LGQRSLP1SLVFLVPVRLNQTV1WDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or imunosuppressive activities. The polypeptides of the invention have an open conformation and are useful a polypeptides of the invention have an open conformation and are useful a mununogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease,
                                     LGGRSLP1SLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                                     1021 VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                                                             TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKO
               LGQRSLPISLVFLVPVRLNQTVINDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                                                                               TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
                                                                        VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF
                                                                                                                                                                                                                                                                                                                                                                                                         Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.
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Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-1 alpha-M protein subunit used to generate the mutant polypeptides of the invention.
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1140 TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140 Beta2 integrin, alphaD subunit, CD11c subunit; CD11b subunit; LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; locomotor impairment; an anti-alpha-d monoclonal antibodies for promoting locomotor ry, inhibiting locomotor damage, limiting locomotor impairment, or a autonomic and sensory dysfunction following spinal cord injury. The invention relates to promoting locomotor recovery, inhibiting altomotor damage, limiting locomotor impairment, or limiting autonomic and sensory distinction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule. The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following LGORSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPV TLPEQGAFVRSQTETKVEPPEVPNDLPLIVGSSVGGLILLALITAALYKLGFFKRQYKD **QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA** LGQRSLP1SLVFLVPVRLNQTV1WDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV VNCSIAVCQRIQCDIPFFGIQEFFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF NVTSENNMPRTNKTERQLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSN autonomic dysfunction; sensory dysfunction; spinal cord injury Human Beta2 integrin alphaCD11b subunit. Example 5; Page 191-194; 270pp; English. Ä. ABG61469 standard; protein; 1153 Van Der Vieren 15-OCT-2001; 2001WO-US032059 13-OCT-2000; 2000US-00688307 MMSEGGPPGAEPQ 1153 (first entry) WPI; 2002-463260/49. Homo sapiens (ICOS-) ICOS Gallatin WM, 27-AUG-2002 18-APR-2002. 901 1 961 1021 1021 1081 1141 901 1081 1141 ABG61469; 196 limiting σĘ ABG61469 RESULT g d ò 요 ò 셤 ò ð ò 

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spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Bera2 integrin alphaD cDNAs and proteins, for use in raising the antibodies. Bera2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory bowel disease, Crohn's disease, ulcerative colitis, immune complex alveolitis and leukaemia. The present sequence is a Bera2 integrin alpha subunit sequence included for comparison with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mac-1; integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related immunological desorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
                                                                                                                                                                                  TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
                                                             NVTSENNMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN
                                                                                                        LGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV
                                                                                                                        VNCSIAVCQRIQCDIPFFGIQEFNATLKGNLSPDWYIKTSHNHLLIVSTAEILFNDSVF
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The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatorid arthritus). The variant integrin I domain proteins and nucleic acids can also be used for treating: ischaemial reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for alpha subunit of integrin
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Best Local Similarity 99.9
Matches 1152; Conservative
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1020 Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CHZ constant region; fall constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent condition; B-cell disorder; melannoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease. The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease. TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD NVTSENNMPRTINKTEFQLELPVKYAVYMVTSHGVSTKYLNFTASENTSRVMQHQYQVSN LGQRSLPISLVPLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV IGORSLPISLVFLVPVRLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV VNCSIAVCORIOCDIPFFGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF TLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLLALITAALYKLGFFKRQYKD UNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVF Binding domain-immunoglobulin fusion protein-associated protein Thompson Disclosure; SEQ ID NO 176; 157pp; English. ¥. Ledbetter JA, Hayden-Ledbetter MS, ADD25615 standard; protein; 1153 17-JAN-2001; 2001US-0367358P. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P. 25-JUL-2002; 2002US-00207655. 1141 MMSEGGPPGAEPQ 1153 1141 MMSEGGPPGÁEPÓ 1153 (first entry) (GENE-) GENECRAFT INC WPI; 2003-801317/75. US2003118592-A1. Inidentified. 15-JAN-2004 26-JUN-2003 1081 901 961 196 1021 1021 1081 ADD25615; 901 ADD25615 RESULT Š õ 셤 ò g ò 셤 à 8

840

QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA 900

LSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS

LSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS

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NCIEDPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD

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disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20000118592. The authors have not identified the sequences in the printed specification by their SBQ ID number therefore none of the sequences can be explicitly identified.
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hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is
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                                                                                                                                                                                                                                                                                       capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polyreptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell alsorder.
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1; Mismatches
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Matches 1152; Conservative
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                                               541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
                                                                                                LSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFDDLSYRKVSTLQNQRS
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                                                                                   DLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK
                                                                                                                                     STRDRLREGQ1QSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP
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469. 471

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693. 695

/label= putative N-glycosylation site

697. 699

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735. 737

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/label= putative N-glycosylation site

1045. .1047

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1051. .1053

/label= putative N-glycosylation site

1076. .11078

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TLLPCQGAFVRSQTETKVEPFBVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140
               Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
                                                                                                                                                                                                                                    Integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant;
                                                                                                                                                                                                                                             osteopathic; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thrombosis; cancer; osteoporosis; sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, e.g. nectanical organ replacement rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
1080 TLPPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD
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                                                                                                               KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN
                                                                                                                                                                                                NTIASKPPRDHVFQVNNFBALKTIQNQLRBKXFAIEGTQTGSSSSFEHEMSQEGFSAAIT
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                                                                                                KKSKTLFSLMQYSEEFRIHFTFKEFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFN
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Score 5930.5; Pred. No. 0; 1; Mismatches

99.6%; ilarity 99.7%; Conservative 1

Best Local Similarity Matches 1150; Conserv

Query Match

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The present invention describes a method (M1) for identifying an inhibitor of HIV entry into a human host cell. (M1) comprises identifying an inhibitor of a cell surface polypeptide selected from CXCR-4 (352.2 anino acids, SEQ ID NO:8, ADP4405), CCR4 (350 amino acids, SEQ ID NO:19, ADP4405), CCR7 (378 amino acids, SEQ ID NO:12, ADP4405), CD1C (1163 amino acids, SEQ ID NO:14, ADP44061), CD47 (323 amino acids, SEQ ID NO:16, ADP44063), CD8 (199 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:20, ADP44071), RARA (162 amino acids, SEQ ID NO:30, ADP44077), CCC (199 amino acids, SEQ ID NO:31, ADP44081), PRXI (150 amino acids, SEQ ID NO:30, ADP44077), CCC (199 amino acids, SEQ ID NO:32, ADP44081), CCC (199 amino acids, SEQ ID NO:32, ADP44081), GRYCA (578 amino acids, SEQ ID NO:32, ADP44081), GRYCA (100 amino acids, SEQ ID NO:30, ADP44081), CCC (100 amino acids, SEQ ID NO:30, ADP44081), GRYCA (100 amino acids, SEQ ID NO:30, ADP44077), GRYCA (100 amino acids, SEQ ID NO:30, ADP44081), GRYCA (100 amino acids, SEQ ID NO:30, ADP44077), GRYCA (100 acids, SEQ ID NO:30, ADP44077), GRYCA (100 acids, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV entry inhibitor; cell surface protein inhibitor; HIV infection; anti-HIV; virucide; HIV uptake inhibitor; human; CD11C; integrin alpha X.
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1141 MMSEGGPPGAEPQ 1153
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N-PSDB; ADP44060.
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ADP 4661

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Query Match 59.0%; Score 3514; DB 8; Length 1163; Best Local Similarity 61.4%; Pred. No. 1.4e-278; Matches 701; Conservative 139; Mismatches 295; Indels 6; Gaps 4;
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VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY

64

1082 1084 PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMMS 1143 RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC 1023 1083 365 485 902 963 124 304 364 424 484 544 604 604 664 664 724 724 784 784 904 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184 67 QCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCP TLPSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA SKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETTSSSSFELEMAQEGFSAVFTPDGP RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYB QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD 665 LLGSRDLÓSSVILDLALDPGRLSPRATFQETKNRSLSRVRVLGLKAHCENFNLLLÞSCVE DPVSPIVLRINFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSW 785 FSFPGLKSLLVGSNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSL 345 RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS ENNMPRTINKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ SIAVCORIQCDIPPEGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP 365 LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE 486 999 725 905 964 245 306 125 485 545 545 605 605 g g 엄 엄 g a 유 ద 8 8 셤 ò a ò 셤 ò ò 요 ઠ ò g ò δ ò ઠે à à ò 셤 ò

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                             ARKNAPKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA
                                                  LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDWNDAYLGYAAAIILRNRVQSLVLGAP
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  PGQEAFWRAQTTTVLEKYKVHNPTPLIVGSSIGGLLLLALITAVLYKVGFFKRQYKEMME 1142
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                                                                                                                                                                                                                                                                                                                                         marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa;
FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; Mip-1(beta);
L-selectin; EGFL6; IDO; IL-8; CD11c; TLR2; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFGSNLRQOPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises marker genes for inflammatory bowel disease (IB) - FcgammaR IIIa, FcgammaR IIIb, Mig, NRG-2, hexokinase, HM74, REG III, LPAP, Mip-1(beta), L-selectin, BGFL6, IDO, IL-8, CD1Lc, and TLR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colltis and Crohn's disease). The present amino acid sequence represents an IBD marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic agent for IBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VLLLTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
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                                                                                                                                                                                                                                                                                                     Human inflammatory bowel disease marker - CD11c protein.
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                                                                                                                                                                                ADN02004 standard; protein; 1163 AA
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                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; ADN01990.
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                                                                               1143
                                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease.
                                         E 1144
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                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not a shown within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                  soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                            Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQFSLMQFSNKFQTHFTFEEFRRTSNPLSLLASVHQLQGFTYTATAIQNVVHRLFHASYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGPT - - QLTQRLPVSRQECPRQEQDIVFLIDGSGSISSRNFATWMNFVRAVISQFQRPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKPPRDHVFQVNNFEALKTIQNQLREKKFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification per se but was submitted in CD format by the inventor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1163;
             - SEQ ID 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3500; DB 8; Length 1
Pred. No. 2e-277;
9; Mismatches 297; Indels
             protein
                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 327; 210pp; English.
            sarcoma-upregulated
                                                                                                                                                                                                   Zlotnik A;
                                                                                                                                                                          (PROT-) PROTEIN DESIGN LABS INC
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                                                                                                                                                   26-NOV-2002; 2002US-0429739P
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            tissue
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                                                                               WO2004048938-A2
                                                         sapiens
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PGQGAFVRSQTETXVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS
                                                                             OTRGGOVSVCPLPRGORARWOCDAVLYGEOGOPWGRFGAALTVLGDVNGDKLTDVAIGAP
                                                                                                                                                         QTRGGQVSVCPLPRGWR-RWWCDAVLYGEQGHPWGRFGAALTVLGDVNGDKLTDVVIGAP
                                                                                                                                                                                                                                   GAOGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD
                                                                                                                                                                                                                                                                                                                           605 GARGOVLLERTRPVLWVGVSMQFIPABIPRSAFBCREQVVSBQTLVQSNICLYIDKRSKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENNTPRISKTTFOLELPVKYAVYTVVSSHEOFTKYLNFSESBEKESHVAMHRYQVNNLGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
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                                                         RYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
                                                                                                                                                                                                             GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
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89. .91
/label= glycosylation site
385. .387
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1050. .1052
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N-PSDB; AAQ06068.
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Clone lambda X47 was isolated from a cDNA library constructed from total RNA extracted from phorbol myristate acetate stimulated HL-60 wells. The library was screened with oligonucleotide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it interacts with TCAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAQ06068, AAR07121-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.) Treatment of viral esp. rhino-viral infection - by admin. of alpha sub-unit of p150.95 cell surface adhesion receptor, opt. together with a beta chain of CD-18 family. Disclosure; Fig 3; 59pp; English

Gaps . 9 Length 1163 Indels 58.6%; Score 3491; DB 2; 61.1%; Pred. No. 1.1e-276; ive 139; Mismatches 299; Local Similarity 61.1%; Proceed 697; Conservative 139; Best Loca Matches

VLLLTALTLCHGFNLDTENAMTFQENARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLY

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QCDYSTGSCEPIRLQVPVEAVNASLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCF 124 67 æ 65

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365 364 424 425 484 485 604 604 664 724 724 784 784 904 963 FSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFFDLDLSYRKVSTLQNQRSQRSW **ARKNAFKILVVITDGEKFGDPLGYEDVIPBADREGVIRYVIGVGDAFRSEKSRQELNTIA** SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP :| |||: |:|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| | RYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE QTRGGOVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAP OTRGGOVSVCPLPRGWR-RWWCDAVLYGEOGHPWGRFGAALTVLGDVNGDKLTDVVIGAP GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV GAQGHVIJLIRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD RLREGOI OSVVTYDLALDSGRPHSRAVFNETKNSTRROTQVLGLTQTCETLKLQLPNCIE DPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT PSFPGLKSLLVGSNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSL SIAVCORIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS ENNMPRINKIEFQLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC PGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMS 128 365 366 486 545 665 845 305 908 425 426 485 545 605 605 725 725 785 785 903 1024 1023 1084 1083 845 905 964 963 ઠે 셤 ò 셤 à 셤 8 g ઠે ద ò ద à g 8 % ð g 8 g \$ B \$ g g 셤 8 ⋧ à 셤 ⋧ 유

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                                                                                                                        RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
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       ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA
                                                                                               SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP
                                                                                                                                                                                        LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                              Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-: diabetees; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11c subunit; rheumatoid arthritis.
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                                                                                                                                                                  Beta-integrin CD11c subunit protein.
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                        AAW65091 standard; protein; 1163
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94US-00286889.
94US-00362652.
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SKPPRDHVFQVNNFBALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP RYQHIGLVAMFRONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE

245 ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA

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**QTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVALGAP** OTRGGOVSVCPLPRGWR-RWWCDAVLYGEOGHPWGRFGAALTVLGDVNGDKLTDVVIGAP GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV

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545 GEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLVDLAV

RLREGGIOSVVTYDLALDSGRPHSRAVFNETKNSTRROTOVLGLTQTCETLKLQLPNCIE 

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605 GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD

664 664 724 724

DPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSIT 784

protein sequence Human

leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11c. macrophage infiltration inhibition; alpha_d integrin;

Homo sapiens

WO200029446-A1

25-MAY-2000

99WO-US027139 16-NOV-1999;

98US-00193043 99US-00350259 16-NOV-1998; 08-JUL-1999;

(ICOS-) ICOS

Van Der Vieren Gallatin MW,

WPI; 2000-387751/33

Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury

Example 5; Fig 1; 270pp; English.

Integring are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11c. This sequence was used in an alignment to identify a novel beta2 integrin alpha (AAA60014 and AAB07359). The present sequence has approximately 66% identify to the protein sequence of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function ag. Type I diabetes, atherosclerosis, miltiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha—d monoclonal antibodies may be used in the inhibition of macrophage infiltration at the site of a central nervous control and antibodies can also be used to detect and system injury. Th diagnose Crohn's

Sequence 1163 AA;

QCDYSTGSCEPIRLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCF 124 64 67 VLILTALTLCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLY Gaps . 9 58.4%; Score 3477; DB 3; Length 1163; 61.0%; Pred. No. 1.5e-275; cive 145; Mismatches 294; Indels 6; Best Local Similarity 61.0%; Pre Matches 696; Conservative 145; ß 65 89 ω Query Match g ઠે g à

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TLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNG 244

completed: January 13, 2005, 15:12:31 ne : 225.571 secs Search cor Job time

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Sequence 176, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 3, Appli
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Sequence 327, App
Sequence 4, Appli
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Sequence 3, Appli
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                                                                                                                         January 13, 2005, 15:13:36 ; Search time 190.522 Seconds (without alignments) 2186.449 Million cell updates/sec
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                                                                                                                                                                                                                                                              1 MALRVLLLTALTLCHGFNLD.......FKRQYKDMMSEGGPPGAEPQ 1153
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-902-481A-5

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 99, Appl
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Sequence 55, Appl
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Sequence 1712, Ap
Sequence 173, Appl
Sequence 1742, Appl
Sequence 1742, Appl
Sequence 1744, Appl
Sequence 1744, Appl
Sequence 1744, Appl
Sequence 1736, Appl
Sequence 1744, Appl
Sequence 1736, Appl
Sequence 1744, Appl
Sequence 1736, Appl
Sequence 103, Appl
Sequence 103, Appl
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## ALIGNMENTS

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                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. US20020062008Alel Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER PILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VOS: 114
SOFTWARE: PATENTIN VET: 2.0
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1; Mismatches
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              Sequence 3, Application US/09350259
Patent No. US20020062008A1
GENERAL INFORMATION:
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99.9%; F
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ORGANISM: Homo sapiens
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US-09-350-259-3
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Qy 1141 MMSEGGPPGAEPQ 1153  Db 1141 MMSEGGPPGAEPQ 1153	RESULT 2 US-09-902-481A-1 Sequence 1, Application US/09902481A Publication No Presonance Add to the Publication of the Publicat	; GENERAL INFORMATION; APPLICANT: Springer, Timothy; APPLICANT: Springer, Motomu	APPLICANT: SITHMAN, JULIA APPLICANT: Mayo, Stephen ; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY ; FILE REFERENCE: A-70586-1/RFY/RMS/RMK	CURRENT APPLICATION NUMBER: US/US/9UZ,48LA CURRENT FILING DATE: 2001-07-09 PRIOR APPLICATION NUMBER: US 60/216,600 PRIOR FILING DATE: 2000-07-07	) NUMBER OF SEQ 1D NOS: / ) SOFTWARE: Patentin version 3.1 ) SEQ ID NO 1 ) LENGTH: 1153	; TYPE: FXI ; FRATURE: ; FRATURE: ; NAME/KEY: mat_peptide	; LOCATION: (17)() ; OTHER INFORMATION: US-09-902-481A-1	Query Match 100.0%; Score 5953; DB 10; Length 1153; Best Local Similarity 99.9%; Pred. No. 0; Matches 1152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy 1 MALRVLLITALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR 60  1 MALRVLLLTALTICHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR 60	Qy 61 GSLYQCDYSTGSCEPIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVK 120	Qy 121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 180  121 GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 180	Qy 181 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFN 240	Qy 241 ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300  241 ITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEL 300.	Qy 301 NTIASKPPRDHVPQVNNFBALKTIQNQLREKKPAIEGTQTGSSSSFEHEMSQEGFSAAIT 360 101 NTIASKPPRDHVFQVNNFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAIT 360	Qy 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420  bb 361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV 420	Qy 421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480  421 LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAP 480	QY         481 HYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEGGQPWGRFGAALTVLGDVNGDKLTDVA 540	Qy 541 IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV 600
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Publication No. US200300772781

GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

APPLICANT: Gallatin, Michael W.

TITLE OF INVENTION: No. US20030077278A1el

CURRENT FILE REFERENCE: 27866/35004

CURRENT FILING DATE: 2001-06-26

PRIOR PELING DATE: 1998-11-16

PRIOR FILING DATE: 1998-11-16

PRIOR FILING DATE: 1994-108-05

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-10-03

PRIOR FILING DATE: 1994-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 1153

TYPE: PRI HOM Sapiens

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APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REPERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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99.9%; Pred. No. 0;
tive 1; Mismatches
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; Sequence 176, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
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Best Local Similarity 99.9
Matches 1152; Conservative
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ORGANISM: Homo
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                                                                                                                                                                                         Sequence 30, Application US/10144259

Publication No. US2003019691A1

GENERAL INFORMATION:

APPLICANT: Arnaout, M. Amin

APPLICANT: Li, Rui

APPLICANT: Xiong, Jian-Ping

ITILE OF INVENTION: VARLANT INTEGRIN POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: 0786-54801

CURRENT APPLICATION NUMBER: US/10/144,259

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR PILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/221,950

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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US-10-144-259-30
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Pred. No. 0;
1; Mismatches
                                                                                                                                                   APPLICANT: Springer, Timothy A.
APPLICANT: Springer, Timothy A.
APPLICANT: Shimaoka, Motomu
APPLICANT: Liu, Chafen
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STR
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STR
TITLE OF INVENTION: DESIRED CONFORMATION AND
FILE REFERENCE: CBN-002CP
CURRENT APPLICATION NUMBER: US 60/229,700
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
SEQ ID NO 4
                                                                                                        Sequence 4, Application US/09945265
Patent No. US20020123614A1
GENERAL INFORMATION:
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Query Match
Best Local Similarity 99.8
Matches 1151; Conservative
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ORGANISM: Homo
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| Sequence 6, Application US/09902481A
| Publication No. US20030054440A1
| General Information:
| APPLICANT: Springer, Timothy
| APPLICANT: Shimmoka, Motomu
| APPLICANT: Shimmoka, Motomu
| APPLICANT: Mayo, Stephen
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| FILE REFERENCE: A-70586-1/RFT/RMS/RMK
| CURRENT FILING DATE: 2001-07-09
| PRIOR FILING DATE: 2001-07-09
| PRIOR FILING DATE: 2000-07-07
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 6
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ORGANISM: Artificial sequence
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Best Local Similarity 99.6'
Matches 1132; Conservative
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US-09-902-481A-6
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SGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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                                                                          SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                                          GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
APPLICANT: MAYO'S tephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT FILING DATE: 2001-07-09
PRIOR PLICATION NUMBER: US 60/216,600
PRIOR PLICATION NUMBER: US 60/216,600
PRIOR PLICATION NUMBER: US 60/216,600
PRIOR PLICATION NUMBER: 3000-07-07
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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; Pred. No. 0;
8; Mismatches
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ORGANISM: Artificial sequence
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99.1%;
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Matches 1127; Conservative
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                                           GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimmacka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ 10 NOS: 7
SOFTWARE: Patentin version 3.1
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98.4%; Score 5859; Di
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1128; Conservative 8; Mismatches
                Sequence 5, Application US/09902481A
Publication No. US20030054440A1
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                               SEQ ID NO 5
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              TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 1137
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Best Local Similarity 98.8
Matches 1123; Conservative
                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
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RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI
                                                                        241 TDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN
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              TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF

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Sequence 3, Application US/09902481A Publication No. US20030054440A1 GENERAL INFORMATION: APPLICANT: Springer, Timothy APPLICANT: Shimmaoka, Motomu APPLICANT: Shifman, Julia

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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glorburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882 0193 NPUSO1
CURRENT APPLICATION NUMBER: US/10/723,860
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SKPPRDHVFQVNNFEALKTIQNQLREKXFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGP
                                                                      RYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYE
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                LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
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; Publication No. US20040253606A1
; GENERAL INFORMATION:
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Publication No. US20030211476A1

GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
TITLE REFERENCE: E1067/20087
CURRENT APPLICANTON NUMBER: 108/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin Version 3.1
FUNDER OF 204
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              GPREFNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASŠTEV
                                                       SGALKSTSCSINHPIPPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTEP
 GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESAS$TEV
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Best Local Similarity 61.3%; Pro
Matches 699; Conservative 139;
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US-10-116-275-204
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   845 HLTCDSAPVG--SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSS
                                    ENDMPRINKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQ
                                                                                                                                                                           SIAVCORIOCDIPFEGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL
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                                                                      ENNTPRISKTTFOLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQ
                                                                                                      RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Alel Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350, 259
CURRENT FILING DATE: 1999-0-08
EARLIER PPLICATION NUMBER: 09/193, 043
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-12-33
EARLIER FILING DATE: 1998-12-33
EARLIER FILING DATE: 1994-12-23
EARLIER FILING DATE: 1994-12-23
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09350259
Patent No. US20020062008A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
                                                  NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                            ; ORGANISM: HOM(
US-10-723-860-327
                                                                                  SEQ ID NO 327
LENGTH: 1163
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125 LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
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RLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIE
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CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
PRIOR PILING DATE: 1994-12-21
PRIOR PLING DATE: 1994-10-03
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
SEQID NOS: 114
                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-891-943-4
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Publication No. US20030077278A1
GENERAL INCOMMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278A1el Human
FILE REFERENCE: 27866/35004
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Job time : 195.522 secs
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Best Local Similarity 59.9%; Pred. No. 6.4e-276;
Matches 683; Conservative 163; Mismatches 287; Indels
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Monica
TITLE CONTROL ON UNC. US2002062008Alel Hum
TITLE REFENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT PILING DATE: 1999-07-08
EARLIER PELLING DATE: 1999-11-16
BARLIER PELLING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/13,497
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATCHIN VOY: 2.0
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Patent No. US20020062008A1
GENERAL INFORMATION:
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-266-889-3
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US-09-183-043-3
US-09-68-307A-3
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US-08-173-497-4

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US-08-485-618-4

US-08-362-652-4

US-08-485-623-4

US-08-482-293A-4

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US-08-173-497-2
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Maximum Match 100%
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Sequence 3, Application US/08173497

Sequence 3, Application US/08173497

Sequence 1 No. 5437958

SEQUENCE 1 INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Van Der Vieren, Monica

TITLE OF INVENTION: Subunit

NUMBER OF SEQUENCES: 29

CORRESSEDE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 S. Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: 111inois

COUNTRY: USA

ZIP: 6066-6402

COUNTRY: USA

ZIP: 6066-6402

COUNTRY: BP PC Compatible

COUNTRY: PC-005/MS-DOS

SOFTWARE: PAPLICATION DATA:

CURRENT APPLICATION UMBER: US/08/173,497

FILING DATE:

CLASSIFICATION: 433

CLASSIFICATION: 433

CLASSIFICATION: 437

CLASSIFICATION: 437

STILING DATE:

CLASSIFICATION: 437
                     US-08-362-652-2

US-08-662-672-2

US-08-602-672-2

US-08-943-363-2

US-09-193-043-2

US-09-688-307A-2

US-09-688-307A-2

US-08-485-618-99

US-08-482-293A-99

US-08-943-363-99

US-08-943-363-99

US-09-1350-259-99

US-09-1350-259-99

US-09-350-253-3

US-08-485-605-618-53

US-08-488-307A-99

US-09-350-259-99
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ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPRA: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, Gerstein, Murray 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATUR SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                 Sequence 3, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, N.
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Fred. No. 0;
1; Mismatches
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REGISTRATION NUMBER: P38,659
REPERENCE/DOCKET NUMBER: 27866/32168
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
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99.9%; F
                                                                                                                                                                                                                                                                                             CITY: Cult.
STATE: Illinois
COUNTRY: United States
7IP: 6606-6402
1141 MMSEGGPPGAEPQ 1153
                                 1141 MMSEGGPPGAEPO 1153
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 1152; Conservative
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-193
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEPP A
REGISTATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        US/08/485,618
                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PATENTIN Release #1
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TELEFAX: 312-474-0448
           CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                    CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 1152; Conservative
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MOLECULE TYPE: protein
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                                   NTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIBGTQTGSSSSFEHEMSQEGFSAAIT
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Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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US-08-485-618-3
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           APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY, AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 312-474-6300
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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Best Local Similarity 99.9
Matches 1152; Conservative
 CURRENT APPLICATION DATA:
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Patent No. 5766850
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850e1 Human 2 Integrin
NUMBER OF SEQUENCES: 93
CORRESPONDENCE MISHAIL, O'Toole, Gerstein, Murray & STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: 111inois
COUNTRY: United States
COUNTRY: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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US-08-362-652-3
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                                       STRDRLKBEGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP
                                                                       NCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDD
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                         STRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Chicago
STATE: 1111inois
COUNTRY: United States
ZIP: 60606-6402
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US-08-605-672-3
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99.9%; Pred. No. 0;
ive 1; Mismatches
             NAWE: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3.
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
ATTORNEY/AGENT INFORMATION:
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Matches 1152; Conservative
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STRANDEDNESS: single
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1; Mismatches
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LENGTH: 1153 amino acids
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Matches 1152; Conservative
                          single
                                                   MOLECULE TYPE: protein
             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                 US-08-482-293A-3
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                                                                    NVTSENNMPRTNKTEFOLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN 960
LSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                781 LSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
                                                      ORSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
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STREET: 233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08482293A, Patent No. 5831029, GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael, APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5831029e1 Human, NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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3R: 27866/32684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
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COUNTRY: United States
ZIP. 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 21-DEC-1994
ATTORNEY/ABENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 27866
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
ITITE OF INVENTION:
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, M. STREET: 233 South Wacker Drive, 6300 Sear;
STREET: 233 South Wacker Drive, 6300 Sear;
STREET: Illinois
STATE: Illinois
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STATE: 105060-6402
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99.9%; Pred. No. 0;
iive 1; Mismatches
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PRIOR APPLICATION DATA:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMERR: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMERR: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams JT: JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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TELEFAX: 312-474-0448
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Best Local Similarity 99.9
Matches 1152; Conservative
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                                                                                   DLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQK
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REPRENCE: 27866/3664
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT PILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/22-22
PRIOR APPLICATION NUMBER: 08/286,89
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
PRIOR PLILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/363,652
PRIOR APPLICATION NUMBER: 08/363,652
PRIOR APPLICATION NUMBER: 08/343,363
PRIOR APPLICATION NUMBER: 08/343,363
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-110-03
NUMBER: PALENTE DATE: 1997-110-03
NUMBER: PALENTE DATE: 1997-110-03
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    TLLPGOGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKD 1140
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99.9%; Pred. No. 0;
ive 1; Mismatches
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Sequence 3, Application US/09193043

Sequence 3, Application US/09193043

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 625139561 Human 2
FILE REFERENCE: 27866/35004

CURRENT APPLICATION NUMBER: US/09/193,043

CURRENT FILING DATE: 1998-11-16

EARLIER FILING DATE: 1994-12-23

EARLIER FILING DATE: 1994-12-21

SERLIER FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114
                                                                                     1141 MMSEGGPPGAEPQ 1153
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Matches 1152; Conservative
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LGÖRSLPISLVFLVPVRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV 1020
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Voeren, Monica
ITILE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350, 259
CURRENT APPLICATION NUMBER: 09/193, 043
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-10-03
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US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
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Best Local Similarity 99.9
Matches 1152; Conservative
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ORGANISM: Homo sapiens
US-09-350-259-3
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99.9%; Pred. No. 0;
iive 1; Mismatches
                                                                                                                    Best Local Similarity 99.9
Matches 1152; Conservative
                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3
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       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
APPLICATION NUMBER: US/08/16,081
FILING DATE: 21-MAX-1991
APPLICATION NUMBER: 07/637,830
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/21,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRAND NUMBER: 29,066
REGISTRAND NUMBER: 29,066
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
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Matches 1149; Conservative
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FRAGMENT TYPE: internal
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                                   361 SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLV
                                                       Sequence 43, Application US/08476062A

Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
CORRESSONDERS: 53
CORRESSONDERS: 53
CORRESSONDERS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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                                                                                                                                                                                                                                                                                                                  Score 5922.5;
Pred. No. 0;
1; Mismatches
                            ATTORNEL FOLLS.

RAME: JOHN W. Freeman
REGISTRATION NUMBER: 29,066
REFREENCE/POCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFRAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.7%;
Matches 1149; Conservative 1
 FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
                                                                                                                             TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                  linear
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PCT-US96-01314-43
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                                                         IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
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SEQUENCE 11 INFORMATION:
APPLICANT: M. Amin Arnaout
ITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
ITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER: U.S.A.
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: PCT/US96/01314
FILLIG DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
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                            IGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLV
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US-08-476-062A-44

i Sequence 44 Application US/08476062A

j Patent No. 5877275

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA
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                                                                           QRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKA
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LSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRS
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Pacent No. 5424399

TILE OF INVENTION: HUMAN CR3a/b HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FILING DATE: 16-JUM-1993

PRIOR APPLICATION NUMBER: 539,842

FILING DATE: 19-JUM-1990

PELLING DATE: 29-JUM-1990

PELLING DATE: 28-JUM-1998
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; Pred. No. 0;
1; Mismatches
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Best Local Similarity 99.7%;
Matches 1149; Conservative
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                                                  505 GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRD
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ZIF: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OMPUTER: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
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GENERAL INFORMATION:
    TITLE OF INVENTION: METHODS FOR IDENT:
    TITLE OF INVENTION: ANTAGONISTS
    NUMBER OF SEQUENCES: 78
    CORRESPONDENCE ADDRESS: 3
    ADDRESSEE: Fish & Richardson P.C. 5
    STREET: 225 Franklin Street
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APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
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STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 VLGAVGSPTWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQSLVLGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIA
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                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      00786/068003
                                                                                                                                                                                   APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1163 amino acids
amino acid
              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-476-062A-44
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Matches 699
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                                                                                                                                                                               Length 1163;
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                                                                                                                                                                             Query Match 58.8%; Score 3500; DB 5; Best Local Similarity 61.3%; Pred. No. 2.3e-279; Matches 699; Conservative 139; Mismatches 297;
                   _29,066
ER: 00786/267001
        NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 00786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEK: 200154
INPORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                         amino acid
                                                                                                                                             ; TOPOLOGY: linear PCT-US96-01314-44
                                                                                                            LENGTH: 1163
                                                                                                                        TYPE: amino a STRANDEDNESS:
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Search completed: January 13, 2005, 15:34:33 Job time : 61.4108 secs

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963
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                                                                                                ENNTPRISKTTFQLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQ
                                                                                                                                 RSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNC
                                                                                                                                                                                SIAVCORIQCDIPPFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLL
                                                                                                                                                                                             RLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTS
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version 5.1.6
- 2005 Compugen Ltd.
  GenCore (c) 1993 .
             Copyright
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protein search, using sw model OM protein January 13, 2005, 15:03:32 ; Search time 5.47465 Seconds (without alignments) 3321.665 Million cell updates/sec Run on:

966 1 CPQEDSDIAFLIDGSGSIIP......FQVNNFEALKTIQNQLREKX 189 RWHU1B-B_COPY_144_332 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62DX Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	0,	Query Match	Query Score Match Length DB	DB	ID	Descript
	996	100.0	1153	-	RWHU1B	cell su
8	746	77.2	1153	~	800551	leukocyt
m	540	55.9		-	RWHU1C	cell sù
4	328	34.0		7	A53213	integri
ហ	287.5	29.8		7	803308	cell su
9	261	27.0		~	156126	lymphoc
7	242	25.1		0	A33809	cartilad

Description	cell surface glyco	cyte su	cell surface glyco	integrin alpha-E c	cell surface glyco	lymphocyte fuction	cartilage matrix p		matrix	lpha 1	_	collagen alpha 1(X	collagen alpha 1(X	integrin alpha-1 c	hypothetical prote	integrin alpha-1 -	integrin alpha-1 c		type XII collagen		collagen alpha 3 (V	collagen alpha 3(V			VLA-2 protein homo	hypothetical prote	undulin 1 - human	collagen alpha 2(V	complement factor
O O	RWHU1B	800551	RWHU1C	A53213	803308	156126	A33809	S66522	A37979	A40020	A45974	S31212	S78476	A45226	S42373	A55348	A35854	T46488	151027	A54849	CGHU3A	A37797	145914	A33998	S44142	T23760	A40970	326	150807
DB	-	~	٦	7	N	~	7	N	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	7	0
Length	1153	1153	1163	1179	1170	1163	493	200	496	3124	1747	1857	1888	1151	3051	272	1180	741	929	2944	3176	3137	1170	1181	1178	250	843	371	763
% Query Match Length	100.0	77.2	55.9	34.0	29.8	27.0	25.1	24.3	24.0	22.3	22.2			21.5		20.4		19.8	19.5	18.1				15.9		15.1		14.5	14.1
Score	996	746	540	328	287.5	261	242	235	232	215	214.5	214.5	214.5	207.5	207.5	197.5	192.5	191.5	188	174.5	164	162	159	154	149	146	143	4	136.5
Bult No.		8	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	52	56	27	58	59

immunodominant mic von Willebrand fac VIA-2 protein - ni	collagen alpha 2(V collagen alpha 2(V collagen alpha 2(V	collagen alpha 2(V collagen alpha 2(V antigen Em100 - Bi	<pre>collagen alpha 2(V collagen alpha 1(V von Willebrand fac</pre>	von Willebrand fac complement factor	hypothetical prote hypothetical prote
A45638 VWHU	\$21369 \$21311 \$04111 \$35243	S09646 CGHU2A A48569	S23377 A32856 G00039	PS0323 BBHU	T28797 T16580
240	4 4 6 6	242	212	7 7	0 0
712 2813	1029 1029 238	917 1018 724	918 1019 427	414 764	567 13055
13.9	13.0	12.7 12.7 12.4	12.3 12.2 12.0	11.7	11.3
134.5	125.5 124.5 122.5	122.5 122.5 119.5	118.5 118 115.5	113.5	109.5 109.5
30	1 W W W 1 W 4 W	36 37 38	39 41	42	44 45

## ALIGNMENTS

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RESULT 1
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N'Alternate glycoprotein CD11b precursor (validated) - human
N'Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Maceukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
cybcocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Cham. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)

A;Reference number: A31108; MUID:88315033; PMID:2457584 A; Accession: A31108

A.Molecule type: mENA
A.Rolecule type: mENA
A.Rolecule type: mENA
A.Rolecule type: 1-1153 <COR>
A.Cross-references: UNIPROT: P11215, GB: J03925; NID: 9187284; PIDN: AAA59544.1; PID: 9307148
A.Note: part of this sequence was confirmed by protein sequencing
A.Note: part of this sequence was confirmed by Drotein sequencing
T. Call Biol. 106, 2153-2158; Pierce, M.W.; Tenen, D.G.
J. Call Biol. 106, 2153-2158; 1988
A.Fitle: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor McA.Reference number: A28915; MuID: 88257215; PMID: 2454931

A; Molecule type: mRNA
A; Residues: 1-499, 501-965, 'P', 967-1153 <ARN>
A; Note: part of this sequence, including the amino end of the mature protein, was confirm R; Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regulates number: A41600, MUID: 92073318; PMID:1683702
A; Accession: A41600
A; Molecule type: DNA
A; Residues: 1-9 <ARD>
A; Accession: A41600
A; Molecule type: CDA
A; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
B; Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
A; Reference number: A41193; MUID:88190151; PMID:2833753
A; Reference number: A41193; MUID:88190151; PMID:2833753
A; Molecule type: DNA
A; Reference number: A1193; MUID:88190151; PMID:2833753
A; Molecule type: Number: May Numb

A; Molecule type: mRNA A; Residues: 917-1042 cAR2> A; Residues: 917-1042 cAR2> A; Residues: 917-1042 cAR2> B; Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989 A; Hitle: CDNA sequence for the alpham subunit of the human neutrophil adherence receptor A; Reference number: A32218; MUID: 89098893; PMID: 2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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N;Alternate names: complement-3 receptor alpha chain
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A,Reference number: A46526; MUID:93123748; PMID:8419480
A,Status: not commandation.
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                                                                                                                                                                                                                                                                   A Molecule type: DNA

A Molecule type: DNA

A Molecule type: DNA

A Molecule type: 1153 <FLE>

A Molecule the last three bases of intron 13, CAG, are included in some but not all mature a Note: the last three bases of intron 13, CAG, are included in some but not all mature a Note: sequence extracted from NCBI backbone (NCBIP:121963)

A Molecule as sequence of the sequence 
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800551
Jeukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
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                                                                                                                                                                                                                   Status: not compared with conceptual translation Molecule type: DNA
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C. Superfamily: cell surface glycoprotein CDilb; von Willebrand factor type A repeat homol C. Superfamily: cell adhesion; glycoprotein; transmembrane protein C. Keywords: cell adhesion; glycoprotein; transmembrane protein P:1-16/Domain: signal sequence #status predicted <SIG> P:1-16/Domain: signal sequence #status predicted <SIG> P:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental P:148-318/Domain: von Willebrand factor type A repeat homology <VWA2> P:1106-1129/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1153 <PVT>
A; Residues: 1-1153 <PVT>
A; Residues: 1-1153 <PVT>
A; Cross-references: UNIPROT: P05555; EMBL: X07640; NID: 952982; PIDN: CAA30479.1; PID: 952983
A; Cross-references: UniPROT: Postor CAC for residue 569 as Gln
A; Note: the authors translated the codon CAC for residue 569 as Gln
A; Note: L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S., 83, 5644-5648, 1986
Proc. Natl. Acad. Sci. U.S., 83, 5644-5648, 1986
A; Titler A partial genomic DNA clone for the alpha subunit of the mouse complement recept
A; Reference number: 159078
A; Reference number: 159078
A; Accession: 159078
                                                                                                                                                                                       chain reveals homology with the ir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
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C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00551; 159078
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                                                                                                                                               R.Pytela, R.
EMBO 0. 7, 1371-1378, 1988
A.Title: Amino acid sequence of the murine Mac-1 alpha 6
A.Reference number: S00551; MUID:88312584; PMID:3044779
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77.2%; Score 746; DB 2;
Best Local Similarity 77.8%; Pred. No. 8.6e-56;
Matches 147; Conservative 20; Mismatches 22
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A, Residues: 1-1163 <COR>
A, Cross-references: UNIPROT: P20702
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C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 20-Feb-1990 #47565; A47565; A48759; S36044
R;Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A;Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit: A;Reference number: S03308; MUID:89139587; PMID:2537322
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A;Residues: 1-1170 <LAR>
A;Residues: 1-1170 <LAR>
A;Residues: 1-1170 <LAR>
A;Cross-treferences: UNIPROT: P20701; UNIPROT: Q9UBC8; EMBL: Y00796; NID: g31421; PIDN: CAA687;
A;Cross-part of this sequence was confirmed by protein sequencing
R;Cornwell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S. 90, 4221-4225; 1993
Proc. Natl. Acad. Sci. U.S. 90, 4221-4225; 1993
A;Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pron
A;Reference number: A47458; MUID: 93248261; PMID: 8097887
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roc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
;Title: Identification of cell-specific and developmentally regulated nuclear factors th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Map position: 16p11.2-16p11.2; Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol; Superfamily: cell surface glycoprotein; heterodimer; surface antigen; trar; 1-25/Domain: signal sequence #status predicted <SIG>; 25/Domain: signal sequence #status predicted <SIG>; 26-1170/Product: leukocyte adhesion glycoprotein LPA-1 alpha chain #status predicted <\ ; 154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell surface glycoprotein CD11a precursor - human
N;Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
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Balo. Chem. 268, 19385-19311, 1993
Title: Characterization of the CD11a (alphaL, LFA-lalpha) integrin gene promoter.; Reference number: A48759; MUID:93374910; PMID:8103515
                                                                                                                                                                                                                  124 GYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQN 183
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                                                                                                                                                              64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL
6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL - - KKSKTLFSLMQYSEEFRIHFTFKEFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB:ITGAL; CD11A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Residues: 1-20 <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-20 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-20 <NUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 QLR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 KLR 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A47458
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A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
C; Map position: 16p1.2-16p1.12
C; Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home C; Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F; 1-19/Pomain: signal sequence #status predicted <81G>
F; 1-19/Pomain: extracellular #status predicted <87T>
F; 100-1107/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 149-319/Domain: transmembrand #status predicted <1NT>
F; 1108-1133/Domain: intracellular #status predicted <1NT>
F; 114-1163/Domain: intracellular #status predicted <1NT>
F; 114-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
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F; 118-1163/Domain: ovn Willebrand factor type A repeat homology <WAA+>
F; 118-1163/Domain f
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                     A; Note: this sequence has been revised in reference A36584
R; Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
BMD J. 6, 4023-4028, 1987
A; Title: CDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A; Reference number: S00864; MUID:88166645; PMID:3327687
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P;199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrin alpha-E chain - human
C;Species: Homo sapiens (man)
C;bate: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C;bate: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C;Accession: A53213
R;Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A;Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit.
A;Reference number: A53213; MUID:94164962; PMID:8119947
                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
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Cross-references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%; Score 328; DB 2; Length 1179; 38.8%; Pred. No. 6e-20;
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A, Map position: 17p13
C, Suberfamilton: 17p13
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Matches 105; Conservative
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Matches 71; Conserv
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Local Similarity
                                                                                                                           A, Accession: A26364
A, Molecule type: mRNA
A, Residues: 78-493 <ARG>
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A;Residues: 1-500 <ASZ>
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Cartilage matrix protein precursor - chicken

Cispecies: Gallus gallus (chicken)

Cispecies: Gallus gallus (chicken)

Cispecies: Gallus gallus (chicken)

Cispecies: Gallus gallus (chicken)

Cispecies: O-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

Cispecies: D-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

Cispecies: D-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

Cispecies: D-Mar-1990 #sequence revision 09-Mar-1990 #text_change matrix protein, a modular protein of the exprise; Von Willebrand factor, complement factors B and C2, and epidermal growth factor. A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Accession: A3809

A; Cossereferences: UNIPROT: P05099; GB:X12346; GB:X12349; GB:X12349; GB:X12355

A; Cross-references: UNIPROT: P05099; GB:X12346; GB:X12347; GB:X12349; GB:X12355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: LFA-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homc
F;151-315/Domain: von Willebrand factor type A repeat homology <VWAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-1163 <RES>
Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156126
R;Kaufmann, Y.; Tseng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit A;Reference number: 156126; MUID:91268576; PMID:2051027
A;Accession: 156126
A;Accession: 15612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFFALKT 180
                                                                                                                                                                                                                                                                        268 TDSGNIDAAKD----IRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKD 322
                                                                                                      EPONNPNPRSLVKPITOLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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; Pred. No. 3.3e-14;
40; Mismatches 72; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphocyte fuction-associated molecule-1-alpha - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 NNFEALKTIQNOLREKX 189
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32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                  181 IQNQLREKX 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFTELOKKI 331
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Best Local Similarity
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A;Cross-references: UNIPROT:P51942; EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163.6; G;Genetics:
A;Genetics:
A;Gene: CMP
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repect; Superfamily: signal sequence #status predicted <81G>P;0-29/Domain: cartilage matrix protein #status predicted <MAT>P;43-210/Domain: von Willebrand factor type A repeat homology <VWAI>P;231-266/Domain: EGF homology <EGF>P;77-441/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                                                                                                  A;Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat; Syperfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat homology <VWA1>
F;237-260/Domain: EGF homology <EGF>
F;235-260/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cartilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66522
Eur. J. Biochem. 236, 970-977, 1996
A;Pitle: Cloning, sequencing and expression analysis of mouse cartilage matrix I
A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 YEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFBALKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F. Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A;Title: Structural features of cartilage matrix protein deduced from cDNA. A;Reference number: A26364; MUID:87092429; PMID:3025875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS--KTLFSLMQYSEEFRIHFTFKEFQN
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29.5%; Pred. No. 1.9e-12;
.ive 45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 25.1%; Score 242; DB 2; Local Similarity 31.2%; Pred. No. 4.8e-13; hes 59; Conservative 39; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Conservative
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Cross-references: EMBL:X67327
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Accession: A40020
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A;Residues: 157-290,'L',292-496 <JE2>
A;Cross_references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g
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collagen alpha 1(XII) chain precursor - chicken
NyAlternate names: fibrochimerin
NyAlternate names: fibrochimerin
Collagen allus gallus (chicken)
Copecies: Gallus gallus (chicken)
Copecies: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
Copecies: No. Sep-1999 *sequence revision 10-Sep-1999 #text change 09-Jul-2004
Copecies: No. Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar J. Cell Biol. 115, 209-221, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe C;Superfamily: cartilage matrix protein; homorrimer F;1-22/Domain: signal sequence #status predicted <SIG> F;23-496/Product: cartilage matrix protein #status predicted <WAT> F;23-406/Product: von Willebrand factor type A repeat homology <WAI>
                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Species: L2-Uul-1991 #sequence_revision 12-Uul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B37979
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; SK-J. Blol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060568; PMID:2246248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
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F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;227-262/Domain: EGF homology <EGF>;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
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24.0%; Score 232; DB 2; Length 496;
Best Local Similarity 29.5%; Pred. No. 3.5e-12;
Matches 56; Conservative 43; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P21941; GB:J05667
A;Accession: B37979
                                                                                                                                                                                                                        A37979
cartilage matrix protein precursor - human
                           180 TIQNQLREKX 189
                                                                                        446 QIGKKLQKQI 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
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A, Molecule type: mRNA
A, Residues: 1-3124 < YAM/
A, Cross-references: UNIPROT: P13944; GB: D00824; NID: G222810; PIDN: BAA00701.1; PID: G222811
A, Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
R; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I)
A, Reference number: A34485; MUID: 90062079; PMID: 2584192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 2772-2792,2846-2873 <GOR2>
R,Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A,Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 2960-2976, Fr, 2978-3074, 'AG' <GOR3>
A; Cross-references: EMBL:M17375, NID:g211649; PIDN:AAA48718.1; PID:g211650
A; Note: this sequence has been revised in reference A34485
R; Koch, M.; Bernasconi, C.; Chiquet, M.
Rix V. Biochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A; Reference number: S23814; WUID:92362621; PMID:1323460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Mesidues: 'X', 1333; 0', 1335-1347; 1914-1928; 2504; 'X', 2506; 'X', 2508-2511; 'X', 2513-2517
A; Molecule type: 'X', 1333; 0', 1335-1347; 1987
J. Biol. Chem. 262, 17724-17727, 1987
A; Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin
                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A34485
A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
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;Title: The two splice variants of collagen XII share a common 5', Title: The two splice variants of collagen XII share a common 5', Reference number: $28811; MUID:93042014; PMID:1420368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P;995-1076/Domain: fibronectin type III repeat homology <PN3G>P;1086-1169/Domain: fibronectin type III repeat homology <PN3H>F;1197-1361/Domain: von Willebrand factor type A repeat homology
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:Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
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F;2899-2901/Region: cell attachment (R-G-D) motif
F;2899-2901/Region: cell attachment (R-G-D) motif
F;2803-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F;2846-3048/Domain: collagenous COL1 #status predicted <COL1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <COL1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3122,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (cova F;2780,2789,2836,2862,2866,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #stat
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C'Species (Gallue gallue)
C'Species (Gallue)
C'Accession: A45974; 830085; 822916; 817035; 820833 #text_change 09-Jul-2004
C'Accession: A45974; 830085; 822916; 817035; 820833 #text_change B.; Cancedda, R.; Lin
KGGERCEK, D.R.; Foley, J.W.; Casteagnala, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
KB. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
fibronectin type III repeat homology <FN3M>
fibronectin type III repeat homology <FN3N>
fibronectin type III repeat homology <FN3N>
fibronectin type III repeat homology <FN3O>
fibronectin type III repeat homology <FN3P>
fibronectin type III repeat homology <FN3P>
fibronectin type III repeat homology <FN3P>
con willebrand factor type A repeat homology <VWA4>
cell adhesion #status predicted
INF, homologous to NC4 domain of type IX collagen #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QDEVEIPARELRNIGVEVFSLGIKAA-----DAKELKLIASQPSLKHVFNVANFDGIV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVME--QLKKSKTLFSLMQYSEEFRIHFTFKEFQ 63
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A;Molecule type: mRNA
A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
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A; Status: preliminary
A; Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Cross-references: UNIPROT: P32018
A; Cross-references: UNIPROT: P32018
A; Experimental source: embryo skin
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
B; Apple, S. S.
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Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 22.3%; Score 215; DB 2; Similarity 30.6%; Pred. No. 9.9e-10; 57; Conservative 37; Mismatches 74;
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                                                                                                                                                              F;2207-2294/Domain: F;2325-2490/Domain: V;2438-2490/Region: C;2509-2750/Domain: I;P;2899-2901/Region: F;2903-2945/Domain: n
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R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F
Bur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens v
A;Reference number: S17035; MUID:92037585; PMID:1935930
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(Skeywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes (Skeywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes F;1-28/Domain: signal sequence #status predicted <SIG>
F;1-28/Domain: signal sequence #status predicted coils f;29-1857/Product: collagen alpha I(XIV) chain, short form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3B>
F;35-433/Domain: fibronectin type III repeat homology <FN3C>
F;35-433/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3D>
F;633-707/Domain: fibronectin type III repeat homology <FN3D>
F;63-707/Domain: fibronectin type III repeat homology <FN3D>
F;741-823/Domain: fibronectin type III repeat homology <FN3E>
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A;Residues: 1-1857 <WAE>
A;Cross-references: EMEL:X70792; NID:g288874; PIDN:CAAS0063.1; PID:g288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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A, Residues: 1472-1659 < GGR1>
A, Residues: 1472-1659 < GGR2>
A, Accession: $20833
A, Molecule type: protein
A, Residues: 1551-1570,1593-1599,1639-1667 < GGR2>
C, Keywords: alternative splicing; coiled coil; extracellular matrix; glycopx C, Keywords: alternative splicing; coiled coil; extracellular matrix; glycopx C, Keywords: alternative splicing; coiled coil; extracellular matrix; glycopx F, 236-317/Domain: fibronectin type III repeat homology < FN3A>
F, 236-317/Domain: fibronectin type III repeat homology < FN3A>
F, 418 + 498/Domain: fibronectin type III repeat homology < FN3C>
F, 706-798/Domain: fibronectin type III repeat homology < FN3C>
F, 716-798/Domain: fibronectin type III repeat homology < FN3C>
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F, 1554-1659/Domain: triple helical domain COLI #status predicted < NC4-
F, 1554-1659/Domain: triple Helical FOLI #status predicted < NC4-
F, 1554-1659/Dom
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFV-STV--MEQLKKSKTLFSLMQYSEEFRIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFRA
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: S31212
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
Bur. J Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%; Score 214.5; DB 2 32.4%; Pred. No. 5.3e-10; tive 31; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Conservative
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Best Local S
Matches 61
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A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F;754-793/Domain: fibronectin type II repeat homology <2F1>
F;1201-1244/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human integrin alpha 1 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                A45226
A45226
A45226
A45226
A5 pecies: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30.Apr.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: A45226
R; Briseswitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 266, 2289-2296, 1993
A; Title: Expression of native and truncated forms of the human integrin alpha 1
A; Reference number: A45226; MuID:93155124; PMID:8428973
A; Accession: A45226
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-1151 cBRI>
A; Cross-references: UMTRROT:P56199
A; Residues: 1-1151 cBRI>
A; Cross-references: UMTRROT:P56199
A; Residues: 1-1151 cBRI>
A; Cross-references: UMTRROT:P56199
A; Residues: 1-1151 cBRI>
A; Cross-reference extracted from NCBI backbone (NCBIP:124326)
B; Ryberimental source: hepatoblastoma CBI backbone (NCBIP:124326)
F; 142-317/Domain: von Willebrand factor type A repeat homology <VWAI>
       1096 KLNAYKTKETLLEAIQQIAYKGGNTKTGKAIKHAREVLFTGEAGMRKGIPKVLVVITDGR 1155
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: S42373
R;Smith, A.
submitted to the BMBL Data Library, March 1994
A;Reference number: S42368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 DIAFLIDGSGSIIPHDFRRMKBFVSTVMEQLK--KSKTLFSLMQYSBBFRIHFTFKBFQN
                                                                         118 KFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEA
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larity 31.5%; Pred. No. 4.2e-09;
Conservative 41; Mismatches 71; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1151;
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A,Residues: 1-3051 <SMI>
A,Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C,Genetics:
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29.8%; Pred. No. 1.2e-09;
tive 39; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.89
Matches 57; Conservative
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A;Residues: 1-1888 cTRU>
A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; PID:g2888
R;Waelchli, C.; Trueb, J.; Keseler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
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F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <WAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
F:35-433/Domain: fibronectin type III repeat homology <FN3B>
F:45-4525/Domain: fibronectin type III repeat homology <FN3C>
F:534-614/Domain: fibronectin type III repeat homology <FN3C>
F:532-707/Domain: fibronectin type III repeat homology <FN3C>
F:41-632/Domain: fibronectin type III repeat homology <FN3C>
F:483-914/Domain: fibronectin type III repeat homology <FN3C>
F:483-914/Domain: fibronectin type III repeat homology <FN3G>
F:483-914/Domain: fibronectin type III repeat homology <FN3G>
F:482-914/Domain: fibronectin type III repeat homology <FN3G>
FN3C-914/Domain: fibronectin type III repeat homology <FN3G-
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C;Date: 11-Mar-1998 #Bequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S78476; S31211
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F;832-914/Domain: fibronectin type III repeat homology <FN3G> F;922-1009/Domain: fibronectin type III repeat homology <FN3H> F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                                                                                              11;
                                                                                                                                            ; Score 214.5; DB 2; Length 1857;
; Pred. No. 5.7e-10;
31; Mismatches 85; Indels 11;
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A;Reference number: S78476
A;Accession: S78476
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Residues: 1-416;1460-1811,1843-1889 <WAE>
:Cross-references: EMBL:X70793
                                                                                                                                        Query Match
22.2%;
Best Local Similarity 32.4%;
Matches 61; Conservative 3:
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1208 FTKIEDEL 1215
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                                                                        623 AILLTDGRSQDNVTGPAD---SARKLSINTFAIGVTDHVLA---SELESIAGSPNR--W 673
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Search completed: January 13, 2005, 15:13:30 Job time : 14.4747 secs

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"CDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
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MEDLINE-89098893; PubMed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
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evolution
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                                                                                                                                                                                                                                                                                                                                                                       rattus
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Q80we9
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ITAL HUMAN
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2: uniprot_trembl:*
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gallus gall
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MEDLINE=88315033; PubMed=2457584;
Gorbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
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MEDLINE-88257215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Manino acquence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
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                                                                                                                                                                                                                                                                                                                                                                                                                              TTAM HUMAN STANDARD; PRT; 1152 AA.
P11215;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1986 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 45, Last annotation update)
101-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1)
(Neutrophil adherence receptor).
Name=1TGAM; Synonyms=CR3A, CD11B;
Homo sapiens (Human).
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                                                                                                                                                                 homo
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                          Q8c270 m
Q951i2 k
P51942 m
Q80vm5 m
P21941 k
Q96dt1 k
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P05099
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                                CAMA CHICK
Q8C270
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CAMA MOUSE
Q80VNS
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Q96DFI
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AAQ88704
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MEDLINE=88190151; PubMed=2833753;
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MEDLINE=93123748; PubMed=8419480;
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GO; GO:0008305; C:integrin complex; TAS.
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InterPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF_A.
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Pfam, PF001839; FG-GAP; 3.
Pfam, PF00092; VWA; 1.
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PDB, 1A8X; Model; Ø=17-1152.
PDB, 1BHO; X-ray; 1/2=-.
PDB, 1BHO; X-ray; 1/2=-.
PDB, 1IDN; X-ray; 1/2=-.
PDB, 1IDN; X-ray; 0=140-331.
PDB, 1IDN; X-ray; 0=143-334.
PDB, 1MU; X-ray; Ø=143-337.
PDB, 1NWZ; X-ray; Ø=144-337.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-335.
PDB, 1NWZ; X-ray; A=140-345.
PDB, 1NWZ; X-ray; A=140-345.
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"Experimental support for a beta-propeller domain in integrin alpha-
"Experimental support for a beta-propeller domain in integrin alpha-
T subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998)

L Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998)

- !- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iG3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen gamma chain.

- SUBGNATT: Hetrodimer of an alpha and a beta subunit. Alpha-M associates with beta-2.

- SUBCELLULAR LOCATION: Type I membrane protein.

- ITSSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: The integrin I-domain (insert) is a VWPA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains I WWPA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl1b.htm".
                                                                                                                                                                                                                         SEQUENCE OF 17-31.
MEDLINE=87076611; PubMed=3539202;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
"N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa.";
Biochim. Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                          Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE-96363371; PubMed=8747460;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99362295; PubMed=9687375; Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairer B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C. S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation model
                       SEQUENCE OF 1-9 FROM N.A.
MEDLINE-92073318; PubMed=1683702;
Shelley C.S., Armaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                   MEDLINE-92144986; PubMed-1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
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 Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)
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MEDLINE=98226734; PubMed=9560195;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00191; Int_alpha; 5.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0244; WWPA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
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REQUENCE FROM N.A. (ISOFORM 2).

REQUENCE FROM N.A. (ISOFORM 2).

REQUENCE FROM N.A. (ISOFORM 2).

REQUENTES 3354683; PubMed=12466851; Adachi J., Bono H., Kondo S.,

RA MEDINIE_25354683; PubMed=12466851; Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Palake J.A., Hill D.P., Bulf C., Hume D.A., Chordench J.,

Baldarelli R., Hill D.P., Bulf C., Hume D.A., Chordench J.,

RA Baldarelli R., Marsuko V., Chothia C., Corbonia C., Corbonia C.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Glssi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Jackson I.J., Jarvis B.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanajaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Kanajaya A., Murcakin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Martais D., Marchionni L., McKenzie L., Miki H.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Saltana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Saltana R., Magner L., Wahlestedt C.A, Setou M., Shimada K.,

RA Varardo R., Wagner L., Wahlestedt C.A, Setou M., Shimada K.,

RA Van Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatuu N.,

RA Shiraki T., Waki K., Kawai J., Arakawa T., Pukuda S.,

RA Hara A., Hashizume W., Imoteani K., Ishii Y., Ilch M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Hara A., Hashizume W., Imoteani K., Ishii Y., Ilch M., Kagawa I.,

RA Hara A., Hashizume W., Imoteani K., Ishii Y., Ilch M., Kagawa I.,

RA Hara A., Hashizahi Y., Sasaki D., Shibata K., Shinagawa I.,

RA Hara A., Hashizahi Y., Sasaki D., Shibata K., Shinagawa I.,
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                     TTAM MOUSE STANDARD; PRT; 1153 AA.
PD5555; Q8CA73;
01-NOV-1988 (Rel. 9, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=88312584; PubMed=3044779;
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MEDLINE=86287312; Pubmed=2942940;
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                                                           181 IQNQLREKX 189
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                                                                                                                                                                      144 CPQEDSDIAFLIDGSGSIIPHDFRRMKBFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFK 203
                                                                                                                                                                                                            EFQNNPNPPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                         204 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
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Subutted (NOV-1995) to the EMEL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                           Length 1152;
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80.4%; Pred. No. 1.5e-54;
Live 19; Mismatches 18; Indels
                                                                       le-69;
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Last annotation update)
                                                           DB 1;
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                                                                           Best Local Similarity 99.5%; Pred. No. 1e-6
Matches 188; Conservative 1; Mismatches
                                                             Score 966;
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                                                           100.08;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit.
Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1153 AA; 127480 MW; 178DB988AECB0343 CRC64;
              Cytoplasmic (Potential). FG-GAP 1.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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                       **Springer T.A., Teplow D.B., Dreyer W.J.;

"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"I alycoproteins and unexpected relation to leukocyte interferon.";

Nature 314:540-542(1985).

"The state of the state of monocytes, macrophages and granulocytes adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. If recognizes Pl and P2 peptides of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in mast cell development and in immune complex-mediated glomerulonephritis, whice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophila ccumulation, in response to a impaired degranulation and phagocytosis, events that the apparently accelerate apoptosis in neutrophils. These mice develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing; Calcium; Cell adhesion;
Direct protein sequecing; Glycoprotein; Integrin; Receptor; Repeat;
Signal; Transmembrane.
SIGNAL 1 16
CHAIN 17 1153 Integrin alpha-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available; TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                    obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P11215; 1BHO.
MGD; MGI:96607; Itgam.
GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:0009185; P:cell adhesion; IMP.
GO; GO:0045123; P:cellular extravasation; IMP.
GO; GO:0030593; P:neutrophil chemotaxis; IMP.
                                                                                                                                                                                                                                                                                                                                                               associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P05555-2; Sequence=VSP_010473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P05555-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000413; Integrin_alpha
InterPro; IPR002035; VWF_A.
              MEDLINE=85188276; PubMed=3887182;
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                               Gaps
                                 Fathallah D.M. Sr., Zerria K. Jr.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
                                                                                                                                                                                                                                                              ;
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                                                                                   GO; GO:0008305; C:integrin complex; IEA.

GO; GO:0007160; P:cell-matrix adhesion; IEA.

GO; GO:000729; P:integrin-mediated signaling pathway; IEA.

GO:000729; P:integrin-alpha.

InterPro; IPR000435; VWF.A.

Ffam; PF00357; Integrin-alpha; 1.

Ffam; PF00357; Integrin-alpha; 1.

Ffam; PF00357; Integrin-alpha; 1.

Ffam; PF00195; VWFADOMAIN.

RRINTS; PR01185; IWTEGRINA.

RRART; SW00191; Int alpha; 5.

SWART; SW00191; INTEGRIN ALPHA; 1.

RROSITE; PS00242; IWTEGRIN ALPHA; 1.

RROSITE; PS00242; IWTEGRIN ALPHA; 1.

RROSITE; PS00242; IWTEGRIN ALPHA; 1.

Cell adhesion; Integrin; Transmembrane.

SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;
                                                                                                                                                                                                                                          Score 719; DB 2; Length 1151;
Pred. No. 1.2e-49;
                                                                                                                                                                                                                                    74.1%; Scor. 74.1%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin alpha-D precursor.
Name=Itgad;
                                                                                                                                                                                                                                                             Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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324 IRNQLQEKI 332
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     NCBI_TaxID=10116;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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60.8%; Pred. No. 1.4e-39;
ive 31; Mismatches 43; Indels
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Extracellular (Potential)
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FG-GAP 2.
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InterPro; IPR000413; Untegrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                   121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                  SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE=96257236; PubMed=8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-235 FROM N.A.
SEQUENCE OF 1-235 FROM N.A.
MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9905942; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S., "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96111956; PubMed=8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
"A_novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoffman P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99370002; PubMed=10438935; Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Garayen M.H., Bochmer B.S., Gallatin W.M., Staunton D.E.; "The leukcoyve integrin alpha D beta 2 blinds VCAM-1: evidence for a binding interface between I domain and VCAM-1."; "Immunol. 163:19984-1990 (1999).

J. Immunol. 163:19984-1990 (1999).
                                                                                                                                                                                                                                                                   05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2)
                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                     PRT; 1162 AA.
                                                                                                                                                                                                                           01349; 015575; 015576;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deta 2-integrin alpha subunit.";
Gene 171:291-294 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunity 3:683-690(1995).
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH VCAM1.
                                                                                                                                  181 IQNQLREKX 189
                                                                                                                                                326 IQRQLQEKI 334
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INTERACTION WITH VCAM1
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                             atherosclerotic plaques, and on splenic red pulp macrophages. DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
                                      associates with beta-2.
SUBCELUILAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell lines and subsets of peripheral blood leukocytes and strongly on tissue-specialized cells, including macrophages foam cells within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                    SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
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Extracellular (Potential)
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GFFKR motif.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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FG-GAP 2.
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
Pfam; PF00092; VWA; INTEGRINA.
PRINTS; PR0185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
SMART; SM00191; VWFADOWAIN.
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EMBL, U40279, AAB60638.1; --
EMBL, H0278, AAB60638.1; --
EMBL, AAB60638.1; JOINED.
EMBL, AF197881, AAF62875.1; --
HSSP, P11215, 1BHO.
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SIGNAL 1 17
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MIM; 602453; -.
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Biol. Chem. 265:2782-2788(1990)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Wistar Kyoto;
Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier
Julier C., Masuda J., Yamori Y., Nara Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59801; AAB03226.1; -.
                                                     Potential
                                                                         Potential)
                                                                                                                                                                                                                                                                                                                                                                              Score 586; DB 1; Length 1162;
Pred. No. 7.7e-39;
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205 AA; 22922 MW; C8C2D9395008DA36 CRC64;
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GHPW -> ATP (in Ref. 2).
L -> V (in Ref. 2).
V -> A (in Ref. 2).
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(GlcNAc. . . )
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Last annotation update)
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; Pred. No. 1.9e-39;
17; Mismatches 24
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                                                N-linked (N-linked                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
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Integrin alpha-M (Fragment)
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61 KVVRELPQKINGARDNAAKILVVITDGEKFGDPLNYEDVIPEAEEAGIIRYVIGVXNAFH 120
90 KVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFR 149
                                                                                                                                                                                                                                                                                                                                                                                                                       Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; "CDNA cloning and complete primary structure of the alpha subunit of laukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                      ITAX HUMAN STANDARD; PRT; 1163 AA.
P20702; QBIVA6;
01-FEB-1991 (Rel. 17, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
01-CCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
11ntegrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CDIIC) (Leu MS).
Name=ITGAX; Synonyms=CDIIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                               :[|:||:||:||:||:
121 KPQSRRELDTIASKPAGDHVFQVDNFEALNTIRNQLQEKI 160
                                                  150 SEKSROELNTIASKPPRDHVFQVNNFEALKTIQNQLREKX 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corbi A.L., Garcia-Aguilar J., Springer T.A.; J. Biol. Chem. 265:12750-12751(1990).
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BEQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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T-S (in Ref. 4).
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                                                                                                                                                                                            209 209 T -> S (in Ref. 4).
251 251 T -> A (in Ref. 4).
490 490 G -> A (in Ref. 4).
547 547 F -> S (in Ref. 4).
556 547 B -> K (in Ref. 4).
556 151 1163 SEK -> TPHYPQDNV (in Ref. 4).
1161 1163 SEK -> TPHYPQDNV (in Ref. 4).
150 157 1 -> V (in Ref. 4).
164 178 180
183 185
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248 249
251 258
269 278
278 269 278
280 291
290 293
313 316
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313 335
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317 AN, 83558A13B5C5DE8F CRC64;
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                                                                                                                                                                                    This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@18b-sib.ch).
                                                                                                       and p150,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383(1987).
-!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.
-!- SUBENIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.
-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
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Extracellular (Potential).
Potential.
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FG-GAP 2.
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FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
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345 IENQLKEKI 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 NFISTSSPLSLLDSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVITDGRKQG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 DNLSYDSVIPWAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFDALKD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPOEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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; Pred. No. 1.3e-34;
33; Mismatches 53; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00242; INTEGRIN ALPHA; UNKNOWN 1.
PROSITE; PS50234; VWFA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%;
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Name=mFLJ00114;
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                                                                                                                                           PRELIMINARY;
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345 IENQLKEKI 353
                IQNQLREKX 189
                                                  325 ÍQNÓLKEKI 333
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                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                181
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285 DNLSYDSVIPMAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFDALKD 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene: The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries."; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c).
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TISSUR=Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
Tsuchiya H.,
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse),
Wararyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.3%; Score 534; DB 2; 54.5%; Pred. No. 1.3e-34; iive 33; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1169 AA.
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103; Conservative
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Strain-129; Tissub-ammary tumor. Brcal-/fl;

KRDINE-2288257; PubMed=12477932;

KRDINE-2288257; PubMed=12477932;

KRJUNE-2288257; PubMed=12477932;

KRJUNE-2288257; PubMed=12477932;

KRJUSHOR R.D., Colling F.S., Margner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Didchenko L., Marusina K., Farmer A.-R., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Carañard T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergere B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                  266 DNLSYDSVIPWAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVFSVENFDALKD 325
          121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=129; TISSUE-Mammary tumor. Brcal-/fl;
Strausberg R.;
Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057200; AAH57200.1; -.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR002035; VWF.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AA; 33404 MW; EC52F3EA48FA068D CRC64;
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                                                                                                                                                                                                                            304 AA
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                                                                                                                                                                                                                                                                Created)
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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Les 80; Conservative
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                                                                                      181 IONOLREKX 189
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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326 IENQLKEKI
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05-JUL-2004
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Q6PG66
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                         PEAM; PPO1839; FG-GAP; 3.
Pfam; PF00357; Integrin alpha; 1.
Pfam; PF00357; Integrin alpha; 1.
Pfam; PF00357; Integrin alpha; 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS00243; VWFA; 1.
Calcium; Call adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%; Score 533; DB 1; Length 1169; 54.5%; Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C616412033C219A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
                                                                                                                                                                                                                                              MGD; MGI:96609; Itgax.
GO; GO:0009897; C:external side of plasma membrane; IDA InterPro; IPR00413; Integrin_alpha.
InterPro; IPR022035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin alpha-X.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential)
FG-GAP 1.
FG-GAP 2.
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By similarity.
By similarity.
By similarity.
By similarity.
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N-linked (GlCNAC.)
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SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
GFFKR motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
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                                                                                                                                                                                                              EMBL; AF211864; AAF23492.1; -.
HSSP; P20702; 1N3Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Signal; Transmembrane
SIGNAL 1 19
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1059
1084
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Local s.
103;
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TRANSMEM
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CARBOHYD
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CA_BIND
CA_BIND
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REPEAT
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SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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PRINTS; PR00453; VWFADOMAIN
    Itgae protein (Fragment).
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                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    EMBL; AF133085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF133075;
AF133076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF133077;
AF133078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF133082;
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AF133081;
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O88340;
01-NOV-1998 (
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN:129; TISSUE=Mammary tumor. Brcal-/fl;

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KA Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Tooshlyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tooshlyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Young A., Sodergren E.J., Lu X., Glbbs R.A.,

Raber J., Helton B., Ketteman M., Green E.D., Dickson M.C.,

Rhiting M., Madan A., Young A., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rad Manner Chuk Generation and initial analysis of more than 15,000 full-length human means and the strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strains and strai
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                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.2%; Score 408; DB 2; Length 304; 53.3%; Pred. No. 5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
Straubberg R.;
Submitted (40G-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057200; AAH57200.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AA; 33404 MW; EC52F3EA48FA068D CRC64;
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Last annotation update)
                                                                                                                                                                                      02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
266 DNLSYDSVIPMAEAASIIRYAIGVGHKDGF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 AA
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                                                                                                                                             304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.3
nes 80; Conservative
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                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                     musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             Integrin alpha X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL--KKSKTLFSLMQYSEEFRIHFTFK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                               Schoen M.P., Arya A., Murphy B.A., Adams C.M., Strauch U.G., Agace W.W., Marsal J., Donohue J.P., Her H., Beier D.R., Olson S., Lefrancois L., Brenner M.B., Grusby M.J., Parker C.M.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
-i- SIMILARITY: Belongs to the integrin alpha chain family.
kukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 895;
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(TrEMBLrel. 08, Last sequence update)
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GO; GO:0007160; P:cell-matrix adhesion; IEA.
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Cell adhesion; Integrin; Transmembrane.
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AAD30063.1; JOINED.
AAD30063.1; JOINED.
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InterPro; IPR002035; VWF_A.
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AAD30063.1; JOINED
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191 EDGTEIAIVLDGSGSIEPSDFQKAKNFISTWMRNFYEKCFECNPALVQYGAVIQTEFDLQ 250
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                                                                                                                         RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA MEDLINE=98058020; PubMed=9394838;

READLINE=98058020; PubMed=9394838;

READLINE=98058020; PubMed=9394838;

RT "Sequence analysis of rat integrin alpha E1 and alpha E2 subunits: rissue expression reveals phenocypic similarities between intraepithelial lymphocytes and dendritic cells in lymph.";

RI Sur. J. Immunol. 27:3070-3079(1997).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the integrin alpha chain family.

DR SMESP; P11215; 1BHQ.

GO; GO:0000305; C.integrin complex; IEA.

DR GO; GO:0007229; P:integrin complex; IEA.

DR GO; GO:0007229; P:integrin—alpha.

DR Pfam; PF001839; FG-GAP; 3.

DR Pfam; PF001839; FG-GAP; 3.

DR Pfam; PF00183; INTEGRIN ALPHA; 1.

DR PRINTS; PR00184; INTEGRIN ALPHA; 1.

DR SWART; SM00191; INTEGRIN ALPHA; 1.

DR SWART; SM00191; INTEGRIN ALPHA; 1.

DR SWART; SM00191; INTEGRIN ALPHA; 1.

DR SWART; SW00191; INTEGRIN ALPHA; 1.
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                   Integrin alpha El.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant; osteopathic; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thromboals; cancer; osteoporoals; sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
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Rabbit be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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                                                                                                                                                                                                                                                                                                           Human integrin alphaM subunit precursor protein.
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17-JUL-2002; 2002US-0396790P.
11-SEP-2002; 2002US-0410135P.
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subunits where one of the subunits has one or more mutations, an altered surface feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-oysteine residue to cysteine or extracellular domains of integrin alpha and beta subunits. The polypeptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic, cytostatic, immunosppressive, antifullammatory, neuroprotective and antisickling activities and may be useful for immunotherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple sclerosis. The current sequence is that of the human integrin alpham subunit precursor protein of the invention.
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Rosenberg S;
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                                                                                                                                                                                                                                                                      Length 1152;
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20-DEC-2002; 2002US-00325899.
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Best Local Similarity
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                                                                                                                                                                                                                                     Sequence 1152 AA,
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Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of

genes

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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic slet, lung, bone marrow or stem cell transplant rejection, rechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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non-specific defence system; integrin gene superfamily.
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Claim 65; SEQ ID NO 2444; 1762pp; English.
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'label= signal_peptide
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                      264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis.
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Pred. No. 2.5e-96;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= putative N-glycosylation site 994. 996. 1996 | 1020. 1024 | 1024 | 1024 | 1024 | 1024 | 1027 | 1047 | 1047 | 1047 | 1047 | 1047 | 1047 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057
                                                    /label= putative N-glycosylation site 901. 903 | 1903 | 1903 | 1904 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 1905 | 19
.abel= putative N-glycosylation site
181. .883
label= putative "
                                                                                                                                                                                                              / nabel = putative N-glycosylation site 941. 943 / label = putative n-glycosylation site
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/label= putative N-glycosylation site
1106. .1134
/label= putative_transmembrane_region
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Matches 188; Conservative 1; Mismatches
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89US-00321239.
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N-PSDB; AAQ04043.
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09-MAR-1989;
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammancyr responses. The present protein sequence is the human integrin alpha subunit collin. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit: alpha (AAA60014 and AAB07359). The present sequence has subunit alpha (AAA60014 and AAB07359). The present sequence has a suproximately 60% identity to the protein sequence of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atheroselerosis, multiple distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system
 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                       264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
                                                                                                                                                                                                                                                                                                                                                     Human; macrophage infiltration inhibition, alpha d integrin;
leukocyte integrin; Leu-CAM; leukointegrin; immune response;
inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
lung inflammation; acute respiratory distress syndrome; Crohn's disease;
rheumatoid arthritis; central nervous system injury; CD11b.
                                                                                                                                                                                                        AAB07360 standard; protein; 1153 AA
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                                                                                                                                                                                                                                                                                                                        Human CD11b protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US027139
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                                                                                                        IONOLREKI 332
                                                                        IQNQLREKX 189
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Length 1153;

Score 966; DB 3; Pred. No. 2.5e-96;

100.0%;

Query Match Best Local Similarity Sequence 1153 AA;

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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immunosuppressive activities. The polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain, and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-I antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the
                                                                                                                            263
                                                                                                                                                          DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                            144 CPOEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSBEFRIHFTFK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified integrin-I or integrin I-like domain polypeptide useful as an immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired
                                                                                          1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 109-112; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human integrin 1 alpha-M subunit protein.
                                                                                                                                                                                                                                                                                                                                         AAU80252 standard; protein; 1153 AA.
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188; Conservative
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binding of an integrin to a cognate ligand such as Crohn's disease, nephritis; human immunodeficiency virus (HIV), myocardial infarction, Sjorgen's syndrome; rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD; leukcyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; inmune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; vascular cecovery; locomotor damage; locomotor impairment; autonomic dysfunction; sensory dysfunction; spinal cord injury.
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The invention relates to promoting locomotor recovery, inhibiting autonomic locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand compart call adhesion molecule, twascular cell adhesion molecule, twascular cell adhesion molecule). The method is useful for promoting component, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alpha cond, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, garfit ather subunit sequence is colitis, immune complex alveolitis and leukaemia. The present sequence is a beta2 integrin alpha subunit sequence included for comparison with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta2 integrin alphaD protein sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1153 AA;
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New integrin I domain protein having alteration in at least 2 noncontiguous regions and exits in an open conformation, useful for treating, preventing or suppressing inflammatory or immunological
                                                                                     Example 1; Fig 1F; 90pp; English.
(BLOO-) CENT BLOOD RES
                               WPI; 2002-148167/19.
                 Springer T;
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The invention comprises structurally biased variant integrin inserted (I) domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins.

The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatoid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating: ischaemia/ repertusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer The variant integrin I domain nucleic acids and infection; and cancer The variant integrin I domain nucleic acids and chective agents. The present amino acid sequence represents the Mac-1 alpha subunit of integrin

Sequence 1153 AA;

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203
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                                                                                                                               EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                             DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                                                                                  144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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Score 966; DB 5; Length 1153;
Pred. No. 2.5e-96;
                                 0; Indels
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1; Mismatches
 100.0%;
99.5%; P
                                 Matches 188; Conservative
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                  Local Similarity
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ADD25615 standard; protein; 1153 AA. (first entry) 15-JAN-2004 ADD25615; 

Binding domain-immunoglobulin fusion protein-associated protein #85.

Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; fimmunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antigon, condition; Becal disorder; melanoma; carctinoma; sarcoma; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.

Unidentified

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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin have region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide comprises: a wild-type human iggin immunoglobulin havy chain CH2 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin hinge region polypeptide comprises: a wild-type human iggil immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human iggil immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human iggil immunoglobulin hinge region polypeptide contains or more cysteine residues, where the mutated human iggil immunoglobulin hinge region polypeptide contains or oysteine residue; and a mutated human iggil immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues are an isolated polymuleotide and contains on antigen. Also included are an isolated polymuleotide encoding the antiging the polymuleotide (operably linked to a promoter), an eccombinant expression construct comprising the polymuleotide (operably linked to a promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct, producing the binding domain-fimmunoglobulin funcion protein, a pharmaceutical composition comprising the binding domain-fimmunoglobulin funcion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, mysthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease, the present sequence is a binding domain immunoglobulin fusion protein-associated protein sequence. Note: The and is also available in electronic formed directly from USPTO electronic formed content of the printed specification and is also available in electronic formed circum mucles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                         Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 176; 157pp; English
                                                                                                                                                                 17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                            25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                 (GENE-) GENECRAFT INC
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-801317/75.
US2003118592-A1.
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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60 ö 0; Indels 100.0%; Score 966; DB 7; 99.5%; Pred. No. 2.5e-96; ive 1; Mismatches 0 Conservative Similarity 188; Query Match Best Local S Matches

Sequence 1153 AA

144 CPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203

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The invention relates to a Factor B analogue that exhibits modified complement activity in vitro. The analogue is generated by substituting a short consensus repeat domain (SCR) or a von Willebrand Factor domain (WP) of human factor B with a SCR or a vWF from a second protein such as human complement activity or an account for substantial tissue damage in a wide variety of autoimmune complex mediated syndromes and mysathenia gravis. Inhibition of the complement system using the analogues is likely to provide a means of the complement system using the analogues. Inhibition of complement may also be favorable in cases that involve tissue damage caused by vascular injury such as myocardial infarction, cerebral vascular accidents or contribute to the destruction of partially damaged tissue as in contribute to the destruction of partially damaged tissue as in reperfusion injury. In addition, the use of complement analogues with cover target specificities could reduce the activity of tissue damaging proteins at sites of inflammation. Complement inhibition is important in the prevention of xenograft rejection (the inhibition of complement by cell-associated and soluble inhibitors is useful in protecting the transplant from damage caused by activation of endogenous complement. The present sequence represents the vWF domain of human factor MAC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Factor B analogue; modified; complement activity; complement factor B; short consensus repeat domain; von Willebrand Factor domain; human; C2; CR3; autoimmune response; tissue damage; lupus erythematosus; therapy; rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1; myocardial infarction; acute shock lung syndrome; inflammation; vWF.
BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                      263
                                                                              DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                     204 EFQNNPNPRSLVKPITQLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                                                     264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding complement protein homologues useful for modulating function of the complement system in the treatment of variety of immune and autoimmune complex mediated syndromes.
                                                                                                                                                                                                                                                                                                                                                                                                                              Human complement factor MAC-1 vWF domain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5A-B; 53pp; English.
                                                                                                                                                                                                                                                                                                       AAY21991 standard; protein; 187 AA
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                                                                                                                                                               IQNOLREKX 189
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                                                                                                                                                                                                                                                                                                                                               AAY21991;
61
                                                                              121
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                                                                                                                                                                                                                                                                RESULT 10
AAY21991
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                                                                                                                                                          BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                            EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                  DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                              121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-11ke domain; inflammacrory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatcory; vasotropic; antiparasitic; vulnerary; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Gly, Ala
/note= "Wild-type Ile substituted by Gly or Ala"
                                                                       ö
                                          Length 187;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human integrin alpha subunit CD11b variant A domain.
                                                                     .
                                                        8.9e-97;
                                          DB 2;
                              99.4%; Scc. 100.0%; Pred. No. 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             AAU76856 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001; 2001WO-US023957
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13-MAR-2001; 2001US-00805354
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
                                                                     Matches 187; Conservative
                                                                                                                                                                                                                                                                            IQNQLRE 187
                                                                                                                                                                                                                                                                                                       181 IQNQLRE 187
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                                                         Local Similarity
               Sequence 187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200209737-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
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                                          Query Match
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CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or conscious 15 and A at residue 320 have been replaced by C, is useful to recidue 315 and A at residue 320 have been replaced by C, is useful cor determining if a test compound to bid by C, is useful compound with the polypeptide and determining if the test compound binds compound with the polypeptide and determining if the test compound binds compound with the polypeptide and determining if the test compound binds compound with the polypeptide and determining if the test compound binds compound with the polypeptide and determining if the test compound binds compound with a integrin polypeptide ligands and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in integrin alpha subunit CD11b variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847

Sequence 191 AA;

120 180 9 9 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVWEQLKKSKTLFSLMQYSEEFRIHFTFK EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG DPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK ö Score 956; DB 5; Length 191; Pred. No. 2.5e-96; 2; Mismatches 99.0%; Matches 186; Conservative IONOLREKX Local Similarity 61 61 121 181 Query Match g ò g ð d ò 요 ઠે

181 İQNQLREKX 189

AAU76847 standard; protein; 191 AA AAU76847; RESULT 12 AAU76847 

(first entry) 21-MAY-2002

Human integrin alpha subunit CD11b A domain.

Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-1ike domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.

Homo sapiens.

Location/Qualifiers Region

.188 /note= "This region is specifically claimed"

WO200209737-A1

07-FEB-2002

31-JUL-2000; 2000US-0221950P. 11-JAN-2001; 2001US-00758493. 13-MAR-2001; 2001US-00805354.

31-JUL-2001; 2001WO-US023957

(GEHO ) GEN HOSPITAL CORP.

Li R, Xiong J; Arnaout AM,

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WPI; 2002-188687/24
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Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.

3xample 2, Fig 5, 55pp, English.

The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by C, or V at residue 313 and A at residue 320 have been replaced by C, or CD1 for determining if a test compound is a candidate compound for binding for determining if a test compound is a candidate compound for binding to the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemia-reperturion injury, immune complexes, restnosts and parasitic diseases, to purify variant integrin polypeptide liqands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit CD11b A domain

Sequence 191 AA;

ö 120 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180 9 61 EFQNNPNPRSLVKPITQLLGRTHIATGIRKVVRELFNITNGARKNAFKLLVVLTDGEKFG 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFK 61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 0; Gaps Query Match 99.0%; Score 956; DB 5; Length 191; Best Local Similarity 97.9%; Pred. No. 2.5e-96; Matches 185; Conservative 3; Mismatches 1; Indels 181 IQNQLREKX 189 엄 ð 셤 Š à ò

181 İQNQLREKI 189

AAB66766

AAB66766 standard; protein; 216 AA. AAB66766;

Amino acids 149-353 of human CR-3 alpha chain and His tag. (first entry) 10-APR-2001

EST; expressed sequence tag; inclusion body; binding partner; immunoglobulins.

Homo sapiens.

Synthetic

WO200102588-A2

30-JUN-2000; 2000WO-EP006137.

99EP-00112815 12-JUL-1999;

(MORP-) MORPHOSYS AG.

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Misc-difference 172
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                                                                                                                        Bajt-Jaeschke ML;
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                                                                                                                                                                                                                                                                                                     Sequence 435 AA;
                                                                                          (UPJO ) UPJOHN
                                                                                                               Heinrikson RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
          WO9529243-A1
                                                  19-APR-1995;
                                                                       26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2002
                              02-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                           99
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                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                    Local
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AAU76866
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                                                                                                  The present invention relates to generating a specific binding partner to a peptide, encoded by a genomic DNA fragment or an expressed sequence tag (EST). A nucleic acid molecule encoding a fusion protein is expressed in a host cell to allow the formation of inclusion bodies comprising the fusion protein, the inclusion bodies are isolated and a specific binding partner is generated. The specific binding partners generated are useful for identifying and characterizing naturally occurring proteins e.g. as immunoglobulins or fragments in immunoassays
                                      Generating specific binding partners to (poly)peptides encoded by genomic DNA fragments, involves forming inclusion bodies by expressing the (poly)peptide as part of fusion proteins.
                                                                                                                                                                                                                                                                                                    PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGY 125
                                                                                                                                                                                                                                                                                                                         131
                                                                                                                                                                                                                                                                                                                                             EDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQVNNFEALKTIGNQL 185
                                                                                                                                                                                                                                                                                                                                                         132 EDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFOVNNFEALKTIONOL 191
                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Spacer
/note= "spacer allows accommodation of Factor-Xa at the
cleavage site"
                                                                                                                                                                                                                                                                                                               PNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKOAFKILVVITDGEKFGDFLGY
                                                                                                                                                                                                                                                            SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                                                        SDIAFLIDGSGSIIPHDFRRMKEFVSTVMBQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukocyte beta-2-integrin Mac-1; I-domain; CD11b; fusion protein; glutathione-S-transferase; GST; Factor-Xa; antiinflammatory.
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                   96.7%; Score 934; DB 4; Length 216; 99.5%; Pred. No. 7.8e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222. .228
/label= Factor-Xa_recognition_sequence
 Von Rueden T;
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                                                                                                                                                                                                                                        1; Mismatches
Hoess A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR77461 standard; peptide; 435 AA.
                                                                                 Disclosure; Page 18; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231. .435
/label= I-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GST-I-domain fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. .221
|abel= GST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
 Kretzschmar T,
                                                                                                                                                                                                                                        Matches 183; Conservative
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                  WPI; 2001-147085/15.
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     REKX 189
                                                                                                                                                                                                                                                                                                                                                                                                          REKI 195
                                                                                                                                                                                                Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage-site
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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12-FEB-1996
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 Frisch C,
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Protein
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A fusion protein comprises a glutathione-S-transferase fusion partner, used to increase the level of soluble protein expression in B. coli and to facilitate affinity purification, and the human leukocyte beta-1 integrin Mac-1 I-domain, linked by Factor-Xa recognition sequence that allows cleavage of the fusion protein and recovery of the I-domain, which is useful as an antiinflammatory. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                             Glutathione-S-transferase fusion protein with Factor Xa cleavage site for prodn. of I-domain from leukocyte B2-integrin Mac-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 EDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 435;
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Pred. No. 2.1e-93;
1; Mismatches 0; Indels
                                                                                                                                                                                                   Fairbanks MB
                                                                                                                                                                                                   Tomich CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 32-34; 41pp; English.
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95WO-US004439.
                                                           94US-00233596
                                                                                                                                                                                                   Anderson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                         WPI; 1995-382991/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the contegrin beta subunit A domain, where I at residue 332 has been replaced by C CDLIb alpha subunit A domain, where I at residue 332 has been replaced by C or varieties 313 and A at residue 320 have been replaced by C, or varieties 313 and A at residue 320 have been replaced by C, is useful to varieties a compound is a candidate compound for binding to CDLIb or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing to the polypeptide. The integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit CDLIb deletion variant A domain. Note: This cariant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
/note= "Wild-type Val substituted by Cys"
                                        /note≈ "Wild-type Ala substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page; 55pp; English
                                                                                                                                                                                                                 31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                                                                                                                                          31-JUL-2001; 2001WO-US023957.
                                                                                                                                                                                                                                                                                                                                                   Arnaout AM, Li R, Xiong J;
                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188687/24
                      Misc-difference 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 177 AA;
                                                                                    WO200209737-A1
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Query Match
92.4%; Score 893; DB 5; Length 177;
Best Local Similarity 97.7%; Pred. No. 1.9e-89;
Matches 172; Conservative 2; Mismatches 2; Indels

Search completed: January 13, 2005, 15:12:32 Job time : 36.3364 secs

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Publication No. US20030078375A1;
GENERAL INFORMATION:
APPLICANT: Arnous, Jan-ping
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Kiong, Jian-ping
ITILE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/805,354
CURRENT PILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/758,493
FRIOR APPLICATION NUMBER: US 60/221,950
PRIOR APPLICATION NUMBER: US 60/221,950
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   RESULT 1
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(c) 1993 - 2005 Compugen Ltd.
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US-09-945-265-4

US-09-902-481A-1

US-09-902-481A-1

US-10-144-259-30

US-10-144-259-30

US-10-207-655-176

US-09-902-481A-6

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ORGANISM: Homo sapiens
US-10-144-259-1
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Sequence 1, Application US/10144259;
Publication No. US20030109691A1
GENERAL INFORMATION:
APPLICANT: Armaout, M. Amin
APPLICANT: Armaout, M. Amin
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00706-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
CURRENT FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2000-07-31
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Sequence 1, Application US/09758493

Publication No. US20040086935A1

GENERAL INFORMATION:

APPLICANT: Arnaout, M. Amin

APPLICANT: Arnaout, M. Amin

APPLICANT: Arnaout, M. Amin

APPLICANT: Xiong, Jian-Ping

TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND

TITLE OF INVENTION: HIGH AFFINITY

TITLE OF INVENTION: HIGH AFFINITY

CURRENT APPLICATION NUMBER: US/09/758,493

CURRENT PILING DATE: 2000-07-31

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 191
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100.0%; Score 966; DB 11; Length 191;
Best Local Similarity 99.5%; Pred. No. 1.6e-93;
Matches 188; Conservative 1; Mismatches 0; Indels 0;
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ORGANISM: Homo sapiens
US-09-758-493-1
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Sequence 4, Application US/09945265

Sequence 4, Application US/09945265

Patent No. US20020123614A1

GENERAL INFORMATION:

APPLICANT: Spiringer, Timothy A.

APPLICANT: Spiringer, Timothy A.

APPLICANT: Spiringer, Timothy A.

TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A.

TITLE OF INVENTION: DESTRED CONFORMATION AND METHODS FOR PRODUCING SAME

FILE REFERENCE: CBN-002CP

CURRENT APPLICATION NUMBER: US/09/945,265

CURRENT PILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: US 60/229,700

PRIOR PILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

SEQ ID NO 4
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Query Match 100.0%; Score 966; DB 14; Length 191; Best Local Similarity 99.5%; Pred. No. 1.6e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0
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US-09-350-259-3
Sequence 3, Application US/09350259
; Patent No. US20020062008A1
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Matches 188; Conservative
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ORGANISM: Homo sapiens
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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRBLFNITNGARKNAFKILVVITDGEKFG 120
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             Query Match
100.0%; Score 966; DB 10; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09891943
; Publication No US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; TITLE OF INVENTION: No. US20030077278A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT FILING DATE: 1996-11-166-26
; PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 09/296,652
; PRIOR FILING DATE: 1994-08-05
; PRIOR FILING DATE: 1994-12-1
; PRIOR APPLICATION NUMBER: 08/362,652
; RIOR FILING DATE: 1997-10-03
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
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ORGANISM: Homo sapiens
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Publication No. US20030054440A1

GENERAL INFORMATION:

APPLICANT: Springer, Timothy

APPLICANT: Shifman, Julia

APPLICANT: Shifman, Julia

APPLICANT: Shifman, Julia

APPLICANT: Mayo, Stephen

TITLE OF INVENTION: NUMBER: US/09/902, 481A

CURRENT FILING DATE: 2001-07-07

PRIOR APPLICATION NUMBER: US 60/216,600

PRIOR PILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1.
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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE CAMT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020662008Alel Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER PILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 08/193,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver: 2.0
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100.0%; Score 966; DB 9;
Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0;
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NAME/KEY: mat_peptide
LOCATION: (17)...()
OTHER INFORMATION:
US-09-902-481A-1
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CORGANISM: Homo sapiens
US-09-350-259-3
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ORGANISM: Homo sapiens
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US-09-902-481A-1
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264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFFALKT 323
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Best Local Similarity 97.4%;
Matches 184; Conservative
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                                 APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Valong, Jian-Ping
FILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-07-31
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 1153
TYPE: PRI SEQ FOR Windows Version 4.0
SEQ ID NO 30
LENGTH: 1153
TYPE: PRI SECONDER: Readelens
VORGANIEM: Homo sapiens
US-10-144-259-30
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Sequence 176, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.;
APPLICANT: Hayden-Ledbetter, Martha S.;
TITLE OF INVENTION: BINDING DOMAIN-IMMUNCGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-401C1
CURRENT APPLICATION UNMER: US/10/207,655
CURRENT PILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426

SOCTWARE: Patentin version 3.0
SEQ ID NO 176
LENGTH: 1153
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Best Local Similarity 99.5%; Pred. No. 1.9e-92;
Matches 188; Conservative 1; Mismatches 0; Indels 0;
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US-10-207-655-176
                   GENERAL INFORMATION:
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61 EPONNDNPRSLVKPITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Springer, Timothy
APPLICANT: Springer, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-07
PRIOR PELIOR DATE: 2000-07-07
SPRIOR PELIOR DATE: 2000-07-07
SPRIOR PELIOR DATE: 2000-07-07
SPRIOR PELIOR DATE: 2000-07-07
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Pred. No. 1.7e-91;
4; Mismatches 1; Indels 0;
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-346-863-37
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CORGANISM: Homo sapiens
US-10-615-515-9
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APPLICANT: Spiringer, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimao, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial sequence
                                         FEATURE:
OTHER INFORMATION: synthetic
US-09-902-481A-5
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                                                                                                                               Query Match
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65 NPNPRSLVKPITQLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
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Pred. No. 8.5e-91;
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Publication No. US20040132974A1;
GENERAL INFORMATION:
APPLICANT: FAGAN, RICHARD, JOSEPH;
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN;
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN;
APPLICANT: GUTTERIOGE, ALEX;
TITLE OF INVENTION: ADHESION MOLECULES;
FILE REFERENCE: 674575-2004;
CURRENT APPLICATION NUMBER: US/10/615,515;
CURRENT PILING DATE: 2003-07-08;
PRIOR FILING DATE: 2003-01-11;
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11;
NUMBER OF SEQ ID NOS: 12;
SOFTWARE: PATENTIN VOIC: 3.2;
SEQ ID NO 9;
FENGINE APPLICATION NUMBER: GB DIO750.9
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: GUTTERLOS, ALEX
TITLE OF INVENTION: ADHESION MOLECTLES
FILE REPERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT APPLICATION NUMBER: PCT/GE01/03318
PRIOR PILING DATE: 2003-01-17
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
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99.5%;
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Best Local Similarity
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NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
                                                                                                                                                                               61 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 120
                                                                                                                                                                                                                                           YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQ 184
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                                                       5 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQN
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            0; Indels
            1; Mismatches
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Fublication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: PRGAN, RICHARD JOSEPH
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR PILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-10-17
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Job time : 32.2304 secs
            Matches 184; Conservative
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; ORGANISM: Homo sapiens
US-10-346-863-17
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LREKI 185
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APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUREY: US
ZIP: 02110-2804
COMPUTER READABLE Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/637,830
FILING DATE: 21-MAR-1991
APPLICATION NUMBER: 07/539,830
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 07/539,830
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 07/539,830
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: 07/539,830
APPLICATION NUMBER: 07/539,830
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APPLICATION NUMBER: 07/539,830
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US-08-482-293A-55
US-08-483-307A-55
US-09-193-043-55
US-09-588-307A-55
US-08-485-618-101
US-08-485-618-101
US-08-485-618-101
US-08-482-293A-101
US-08-943-363-101
US-08-193-043-101
US-09-183-043-101
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US-08-183-043-101
US-08-183-043-101
US-08-186-889-46
US-08-485-618-46
US-08-485-618-46
US-08-485-618-46
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REGISTRATION NUMBER: 29,066
REPERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 8EQUENCE CHARACTERISTICS:
LENGTH: 1152 amino acids
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
  TYPE: amino acid
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STATE: MA
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('Ggn2_6')todata1/|iaa/PCTUS_COMB.pep:*

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                         version 5.1.6
- 2005 Compugen Ltd.
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US-08-173-497-3

US-08-18-618-3

US-08-362-652-3

US-08-362-652-3

US-08-605-672-3

US-09-193-043-3

US-09-193-043-3

US-09-193-043-3

US-09-193-043-3

US-09-193-612-5

PCT-US95-04439-1

US-08-485-518-3

US-08-485-618-37

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US-08-485-618-37

US-08-605-672-37

US-08-943-33-37
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PCT-US96-01314-43
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US-09-350-259-37
US-08-485-618-55
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
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Maximum DB seq length: 200000000
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No.
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204 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                       121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
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                                                                                       264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFOVNNFFBALKT
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233 S. Wacker Drive, 6300 Sears Tower
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               5424329---
; Patent No. 5424399
; PATELE OF INVENTION: HUMAN CR3a/b HETERODIMERS
ITILE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1996
; PADLICATION NUMBER: 212,573
FILING DATE: 28-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 966; DB 6; 99.5%; Pred. No. 5.2e-93; ive 1; Mismatches 0;
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Patent No. 5437958
GENERAL INFORMATION:
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: Subunit
TITLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5
Matches 188; Conservative
                                                                                                                                                        181 IQNQLREKX 189
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STREET: 233 S.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-173-497-3
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                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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  Length 1152;
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                                                  0; Indels
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GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCES: 78
CORRESPONDENCES: Fish & Richardson P.C.
STREET: 225 Franklin Street
100.0%; Score 966; DB 2; 99.5%; Pred. No. 5.2e-93;
                       Pred. No. 5.2e
1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: MASBAGINGELES
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IEM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-UAN-96
PRIOR APPLICATION NUMBER: 08/380,167
FILING DATE: 30-UAN-95
ATTORNEY AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
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Conservative 1;
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                       Best Local Similarity 99.5
Matches 188; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 188; Conserv
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PCT-US96-01314-43
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TELEX: 2'
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Query Match
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61 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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STATE: 111inois
COUNTRY: United States
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
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REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
         TELECOMMUNICATION INFORMATION:
                                              TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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US-08-485-618-3
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Sequence 3, Application US/08286889
September 10.5470953
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September 10.54709530
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
APPLICATION DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKEY NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6448
TELEFAX: 312-474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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CITY: Chicago
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                          100.0%; Score 966; DB 1; Length 1153; 99.5%; Pred. No. 5.2e-93; tive 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                      1153 amino acids
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        Matches 188; Conservative
            SEQUENCE CHARACTERISTICS
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                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-362-652-3
                                                                                    single
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                                                          TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                 Local Similarity
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US-08-605-672-3
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Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                      Score 966; DB 1; Length 1153; red. No. 5.2e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 213 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                       0; Indels
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
                                                                                                                                                                                                                                                                                                                                Pred. No. 5.2e
1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DBC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,686,897
REGISTRATION NUMBER: 38,686,897
FILING STRATION NUMBER: 38,686,897
FREGISTRATION NUMBER: 38,686,897
FREGISTRATION NUMBER: 38,687
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.5%;
Matches 188; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312-474-6300
312-474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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                                                                                                                                                                                                          Gaps
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Patent No. 5837478

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INFORMICS: 114
CORRESPONDENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bornn
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                                                                                                                                                 Query Match 100.0%; Score 966; DB 2; Length 1153; Best Local Similarity 99.5%; Pred. No. 5.2e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FOLDER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
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COMPUTER: IBM PC COMPATIBLE
APPLICATION NUMBER: US/08/943,363
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELERRAN: 312-474-6300
TELERRAN: 312-474-6300
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
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                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                              144 CPQEDSDIAFLIDGSGSIIPHDFRRMKBFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                                                             204 BPQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
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Sequence 3, Application US/08482293A

Patent No. 5831029

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Geretein, Murray & Borun
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                                                                                                                                                                          Query Match 100.0%; Score 966; DB 2; Length 1153; Best Local Similarity 99.5%; Pred. No. 5.2e-93; Matches 188; Conservative 1; Mismatches 0; Indels 0;
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
PILING DATE: 23-DEC-1993
PRIOR APPLICATION UNBAR:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 27866
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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INFORMATION FOR SEQ ID NO: 3:
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1153 amino acids
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                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3
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324 IQNQLREKI 332
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CITY: Chicago
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RESULT 12
US-09-688-307A-3
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                                                                                       ; Score 966; DB 2; Length 1153; Pred. No. 5.2e-93; 1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1998-11-16
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09193043
Patent No. 6221395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 625139561 Human 2
PILE REFERENCE: 27866/35004
                                                                                       Query Match
Best Local Similarity 99.5%;
Matches 188; Conservative 1
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SEQ ID NO 3

LENGTH: 1153

TYPE: PRT

CORGANISM: Homo sapiens

US-09-193-043-3
                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-943-363-3
STRANDEDNESS: single
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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APPLICANT: Gallatth, michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REPERENCE: 27866/3646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR PILING DATE: 1993-12-23
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-10-03
PRIOR PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NOS: 114
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Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0;
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GENERAL INFOGRATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITIE OF INVENTION: NO. 6620915el Human 2
FITIE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350, 259
CURRENT FILING DATE: 1999-07-08
EARLIER PELLICATION NUMBER: 09/193, 043
EARLIER APPLICATION NUMBER: 08/173, 497
EARLIER APPLICATION NUMBER: 08/266, 889
EARLIER APPLICATION NUMBER: 08/266, 889
EARLIER PELLING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362, 652
EARLIER APPLICATION NUMBER: 08/362, 652
EARLIER APPLICATION NUMBER: 08/362, 652
EARLIER APPLICATION NUMBER: 08/362, 652
Sequence 3, Application US/09688307A Patent No. 6432404
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                                                        GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
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; ORGANISM: Homo sapiens
US-09-688-307A-3
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                            61 EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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                                                                       1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBFRIHFTFK
       0; Gaps
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       0; Indels
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APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GOORTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26-JUL-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION SITE
APPLICATION NUMBER: US/08/177,109
FILING DATE: US/08/177,109
FILING DATE: US/08/177,109
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FILING DATE: US/08/177
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100.0%; Pred. No. 2e-93;
iive 0; Mismatches 0
       0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5928892
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 amino acids
amino acid
       Matches 187; Conservative
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Matches 187; Conservative
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US-08-687-706-61
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
SECTIANCE STEEM: PC-DOS/MS-DOS
CURRENT APPLICATION DAR: 103-4N-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pablet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/08171109A
Patent No. 5865615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 966; DB 4;
Best Local Similarity 99.5%; Pred. No. 5.2e-93;
Matches 188; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patrea L. Pabst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (404) 873-8795 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 187 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 IQNQLREKI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IONOLREKX 189
                                                                                             , SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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Db 61 EFQNNPNPRSLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
Qy 121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Qy 181 IQNQLRE 187
Db 181 IQNQLRE 187
Search completed: January 13, 2005, 15:34:34
Job time: 10.0829 secs
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5.1.6
Compugen Ltd.
version :
GenCore
(c) 1993
       Copyright
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- protein search, using sw model OM protein January 13, 2005, 15:03:32 ; Search time 5.12706 Seconds (without alignments) 3321.665 Million cell updates/sec Run on:

RWHUIB-C_COPY_144_320 Perfect score:

922 1 CPQEDSÖIAFLIDGSGSIIP......NTIASKPPRDHVFQCNNFEC/177 Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult		ָ קיק קיק				
No.	Score		ength	DB	Ω	Descri
-	903	:	1153	<u>.</u> -	RWHU1B	cell g
7	692	75.1		~	800551	lenko
٣	486	52.7	1163	н	RWHU1C	cell s
4	309	33.5		~	A53213	integr

Description	cell surface glyco	ಹ	grin alpl	cell surface glyco	ű n	cartilage matrix p	matrix	cartilage matrix p	ot	collagen alpha 1(X	collagen alpha 1(X	collagen alpha 1(X	collagen alpha 1(X	integrin alpha-1 c	hypothetical prote	integrin alpha-1								U	hypothetical prote	ha	immunodominant mic	von Willebrand fac
ID	RWHU1B	RWHU1C	A53213	803308	156126	A33809	S66522	A37979	S42373	A45974	831212	S78476	A40020	A45226	T46488	A55348	A35854	151027	A54849	I45914	A37797	A33998	CGHU3A	S44142	T23760	S32604	A45638	VWHU
DB		۰,	7	~	~	~	N	N	N	~	N	N	~	~	~	N	N	~	N	~	~	~	N	N	7	~	~	Н
Length	1153	1163	17	17	1163	σ	200	496	3051	1747	1857	1888	3124	1151	741	272	1180	929	2944	1170	3137	1181	3176	1178	550	371	712	2813
Query Match	97.9	52.7	8	28.8	56.6	24.6	24.1	23.3	21.3	21.1	21.1	21.1	ö		19.5	19.1	18.6	17.8	17.1	16.4	•	15.6	15.6	15.3	15.0	14.8	14.6	14.3
Score	903	486	309	265.5	245	227	222	215	196.5	194.5	194.5	194.5	192	186.5	179.5	176.5	171.5	164	157.5	151	150.5	144	144	141	138	m	134.5	132
sgult No.	-10	a m	4	ß	9	7	∞	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29

undulin 1 - human	complement factor	collagen alpha 2(v	VLA-2 protein - pi	collagen alpha 2(V	antigen Em100 - Ei	collagen alpha 2(V	collagen alpha 2(V	collagen alpha 2(V	collagen alpha 2(V	collagen alpha 1(V	von Willebrand fac	von Willebrand fac	hypothetical prote	hypothetical prote	collagen alpha 1(V
A40970	I50807	S04111	147230	S21369	A48569	C35243	S09646	CGHU2A	S23377	A32856	G00039	PS0323	T28797	T16580	S34839
7	N	~	~	Н	~	N	~	-	N	н	7	~	~	~	0
843	763	1022	191	1029	724	238	917	1018	918	1019	427	414	567	13055	1025
13.9	13.8	13.5	13.2	13.1	13.0	13.0	13.0	13.0	12.9	12.7	12.5	12.3	11.9	11.8	11.5
128	127.5	124.5	121.5	121	120	119.5	119.5	119.5	118.5	117	115.5	113.5	109.5	108.5	106

## ALIGNMENTS

RWHUIB
cell surface glycoprotein CD11b precursor [validated] - human
NyAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimotc, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)

A; Reference number: A31108; MUID:88315033; PMID:2457584

A,Accession: A31108
A,Molecule Krype: mRNA
A,Residues: 1-1153 <COR>
A,Residues: 1-1153 <COR>
A,Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A,Note: part of this sequence was confirmed by protein sequencing
A,Note: part of this sequence was confirmed by Drotein sequencing
A,Aranout, M.A.; Gupta, S.K.; Pierre, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A,Title: Anino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mc
A,Reference number: A28915; MUID:88257215; PMID:2454931

A; Molecule type: mRNA
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confirm R; Shelley, C.S.; Arnaout, M.A.
R; Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg.
A; Reference number: A41600; MUID:92073318; PMID:1683702

A; Molecule type: DNA A; Residues: 1-9 < SHE>

A,Cross-references: GB:W76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R;Arnaout, M.A.; Remold-O'Donnell, B.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85; 2776-2780, 1988
A;Title: Wolecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic A;Reference number: A94193; WUID:88190151; PMID:2833753

A;Molecule type: mRNA A;Residues: 917-1042 <AR2>

A,Cross-references: GB:M18044
R,Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Rrickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A.F.C. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A,Title: cDNA sequence for the alpham subunit of the human neutrophil adherence receptor A,Reference number: A32218; MUID:8909883; PMID:2563162
A,Accession: A32218

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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R;Corbi, A.L.; Garcia-Aguilar, J.; Sp)
J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
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A,Molecule type: DNA
A,Residues: 1-1163 <COR>
A,Cross-references: UNIPROT: P20702
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Best Local Similarity 77.39
Matches 136; Conservative
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A; Residues: 1-834 < CO2>
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A; Map position: 16p11.2-16p11.2
A; Note: promoter contains a GATA motif and two Sp1 consensus binding sites
A; Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C; Superfamally: cell surface glycoprotein CD1b; von Willebrand factor type A repeat home
C; Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C; Reywords: alternative splicing; calcium; predicted <STG>
F; 1-16 / Domain: signal sequence #status predicted <STG>
F; 1-1108 / Domain: signal sequence glycoprotein CD1b #status experimental <MAT>
F; 17-1108 / Domain: extracellular #status predicted <ATY>
F; 17-1108 / Domain: calcium/magnesium binding #status predicted
F; 530-538 / Region: calcium/magnesium binding #status predicted
F; 530-601 / Region: calcium/magnesium binding #status predicted
F; 1109-1134 / Domain: intracellular #status predicted <TWM>
F; 1109-1134 / Domain: intracellular #status predicted <INT>
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F; 1135 / Domain: intracellular #status predicted <INT>
F; 1135 / Domain: intracellular #status predicted <INT>
F; 1135 / Domain: intracellular #status predicted <INT>
F; 1135 / Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: protein
A; Residues: 17-31 < PIE>
A; Residues: 17-31 < PIE>
A; Residues: 17-31 < PIE>
A; Experimental source: granulocytes
B; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A; Title: Characterization of the myeloid-specific CD11b promoter.
A; Reference number: I52567; MUID:92144986; PMID:1346576
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-9 < RES>
A; Cross-references: GB: M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C; Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
                                                                                                                                             gene and phylogenetic analysis of the alpha-in
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A;Note: the last three bases of intron 13, CAG, are included in some but not all mature A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Pierre, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across spacerence number: A90664; MUD:87076671; PMID:3539202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Rifleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G. J. H. A. 1993
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                                                                                                                                    A, Title: Structural analysis of the CD11b gene and phylon during evolution.
A, Reference number: A46526; MUID:93123748; PMID:8419480
                                                                                                                                                                                                                                                                             A, Molecule: not compared with conceptual translation A, Molecule type: DNA A, Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:120599; OMIM:120980
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                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-499,501-1153 <FLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: ITGAM; CR3A
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EMBO J. 7, 1371-1378, 1988
A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
A;Reference number: S00551; MUID:88312584; PMID:3044779
A;Accession: S00551
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1153 <PYT>
A; Residues: 1-1153 <PYT>
A; Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Note: the authors translated the codon CAC for residue 569 as Gln
R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
A; Reference number: 159078; MUID:86287312; PMID:2942940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AjGene: Mac-1

(Subperfamily: cell surface glycoprotein; transmembrane protein

C;Superfamily: cell adhesion; glycoprotein; transmembrane protein

C;Keywords: cell adhesion; glycoprotein; transmembrane protein

F;1-16/Domain: signal sequence #status predicted <SIG>

F;1-15/Product: leukcoyte surface glycoprotein Mac-1 alpha chain #status experimental

F;18-118/Domain: von Willebrand factor type A repeat homology <WWA2>

F;1106-1129/Domain: transmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A;Reference number: A35543; MUID:90153906; PMID:2303426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EFONNPNPRSLVKPITQLLGRIHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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NiAlternate names: leukocyte adhesion receptor p150,95 alpha chain
CiSpecies: Homo sapiens (man)
CiDate: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
CiAccession: A36584; A35543; S00864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 11-44 <RES>
A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1153;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.1%; Score 692; DB 2, 77.3%; Pred. No. 3e-53; iive 18; Mismatches
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fuction-associated molecule-1-alpha - mouse
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Matches 58; Conservative
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A; Residues: 1-20 < COR>
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Residues: 1-20 <SHE>
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A;Residues: 1-20 <NUE>
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A; Map position: 16p11_2-16p11.2
A; Map position: 16p11_2-16p11.2
A; Map position: 16p11_2-16p11.2
A; Map position: 16p11_2-16p11.2
A; Map position: 16p11_2-16p11.2
A; Map position: 16p11_2-16p11.2
B; Demain: 201cum; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; E; 1-19/Domain: signal sequence #status predicted <SIG>
E; 1-19/Domain: stracellular #status predicted <SIG>
E; 0-1103/Domain: von Willebrand factor type A repeat homology <VWA4>
F; 1108-1133/Domain: transmembrane #status predicted <TWA>
F; 1108-1133/Domain: transmembrane #status predicted <IVA>
F; 1149-319/Domain: theracellular #status predicted <IVA>
F; 1149-319/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA>
F; 1184-1163/Domain: ditracellular #status predicted <IVA
F; 1184-1163/Domain: ditracellular #status predicted <IVA
F; 1185-1165/Domain: ditracellular #status predicted <IVA
F; 1185-1165/Domain: ditracellular #status predicted <IVA
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F; 1185-1165/Domain: ditracellular #status predicted <IVA
F; 1185-1165/Domain: d
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A;Map position: 17p13
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
F;199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                      Ę
A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB.MB1695; EMBL.Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M. J. Biol. Chem. 269, 6016-6025, 1994
A;Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. A;Reference number: A53213; MUID:94164962; PMID:8119947
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C;Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
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A;Residues: 1-1179 <SHA>
A;Cross-references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245
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                                                                                                                                                                              A; Gene: GDB: ITGAX; CD11C
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Best Local Similarity
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A, Status: preliminary
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Cell surface glycoprotein CD11a precursor - human NyAlternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function Cispecies: Homo sapiens (man)
C; paceiss: Homo sapiens (man)
C; pate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Ju1-2004
C; pacession: S03308, A47458; A47755; A487759; S36044
E; Larson, R.S.; Corbi, A.L.; Barman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A; Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit: A; Reference number: S03308; MUID:89139587; PMID:2537322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: part of this sequence was confirmed by protein sequencing
R;Cornwell, R.D.; Gollahon, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. US.A. 90, 4221-4225, 1993
A;Titler Description of the leukocyte function—associated antigen 1 (LFA-1 or CD11a) pron
A;Reference number: A47458; MUID:93248261; PMID:8097887
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R;Shalley, CS.; Farckhzad, O.C.; Armaout, M.A.
Proc. Mail. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A;Title: Identification of cell-specific and developmentally regulated nuclear factors the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of th
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F;26-1170/Product: leukcoyte adhesion glycoprotein LFA-1 alpha chain #status predicted <A F;154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
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R;Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Balol. Cham. 268, 19305-19311, 1993
A;Title: Charcrization of the CD11a (alphal, LFA-ialpha)
A;Reference number: A48759; WUID:93374910; PMID:8103515
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Accession: A47565
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A;Residues: 1-1170 <LAR>
A;Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8;
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A;Cross-references: GDB:119757; OMIM:153370
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K;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shc J. Biol. Chem. 265, 19624-19631, 1990
A;Fitle: Structure and chromosomal location of the human gene encoding cartilage matrix I A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein precursor - mouse C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S6652
R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Bur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein ct
A;Reference number: S66522; MUID:96270751; PMID:8665920
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A;Gross-references: GB:M55603; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A reper F;1-29/Domain: signal sequence #status predicted <SIG> F;30-500/Product: cartilage matrix protein #status predicted <MAT> F;43-210/Domain: von Willebrand factor type A repeat homology <VWAl> F;231-266/Domain: EGF homology <EGF> F;237-441/Domain: von Willebrand factor type A repeat homology <VWAl>
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                                65 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG 124
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C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B379799
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTL--FSLMQYSEEFRIHFTFKEFQ
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                                                                                                                                                                                   386 -QDYITDAAKKAKDLGFRMFAVGVGNAV----EDELREIASEPVAEHYFYTADF
                                                                                                                                            125 YEDVIPEADRE----GVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQCNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.1%; Score 222; DB 2; Length 500
Best Local Similarity 30.5%; Pred. No. 5.9e-12;
Matches 54; Conservative 39; Mismatches 66; Indels
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A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941; GB:J05667
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A;Map position: 1p35-1p35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage matrix protein precursor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Accession: 866522
;Status: preliminary
;Molecule type: mRNA
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                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1163 <RES>
A;Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g198786
                                                                                                                                                                                                                                                                                                                                         A;Gene: LFA-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
F;151-315/Domain: von Willebrand factor type A repeat homology <VWAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage matrix protein precursor - chicken
(Species Gallue gallue (chicken)
(Species Gallue gallue (chicken)
(Species Gallue gallue (chicken)
(Species Gallue gallue (chicken)
(SAccession: A33809; A26364
(A261)
(A261)
(A33809; A26364
(A261)
(A33809; A26364
(A33809; A33809; A33809; A33809; A33809; A33809; A33809; A340)
(A33809; A33809; A33809; MUID:89255246; PMID:2542265
(A33809; MUID:89255246; PMID:2542265
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A; Residues: 1-493 <KIS>
A; Residues: 1-493 <KIS>
A; Cross-references: UNIPROT: P05099; GB: X12346; GB: X12347; GB: X12348; GB: X12349; GB: X1235
R; Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A; Title: Structural features of cartilage matrix protein deduced from cDNA.
A; Reference number: A26364; MUID: 87092429; PMID: 3025875
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                                                  R;Kaufmann, Y.; Tseng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit
A;Réference number: I56126; MUID:91268576; PMID:2051027
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A;Rosaidues: 78-493 - ARG>
A;Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A:
F;37-204/pomain: von Willebrand factor type A repeat homology <VWAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : |: || || || || || CMKGKVDLVFLFDGSQSLDRKDFBKILEFMKDVMRKLSNTSYQFAAVQFSTDCRTEFTFL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EF-QNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS--KTLFSLMQYSEEFRIHFTFKEFQN 64
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156126
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F;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 245; DB 2; Length 1163;
Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Mismatches
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ilarity 32.6%;
Conservative 33
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Best Local Similarity
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Best Local (
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rwhulb-c_copy_144_320.rpr

regions

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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 286-494 'O, 496-834 'A', 836-1119, 'KL', 1122-1402,1409-1439 <TRU>
R;Residues: 286-494 'O, 496-834 'A', 836-1119, 'KL', 1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F
Rur. J, Blochen. 201, 333-338, 1991

Rur. J, Blochen. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens v
A;Reference number: S17035; MUID:92037585; PMID:1935930
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A/Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A/Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A/Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C/Rewords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimes of the constant of the coil is coiled to coil; extracellular matrix; glycoprotein; trimes of the coiled to main: von Willebrand factor type A repeat homology <WN3A>
F/236-107/Domain: fibronectin type III repeat homology <WN3B>
F/418-498/Domain: fibronectin type III repeat homology <WN3D>
F/527-007/Domain: fibronectin type III repeat homology <WN3B>
F/257-007/Domain: fibronectin type III repeat homology <WN3C>
F/24-1089/Domain: von Willebrand factor type A repeat homology <WN3C>
F/24-1089/Domain: non-collagenous NC2 #status predicted <NC3>
F/111-1352/Domain: non-collagenous NC2 #status predicted <NC3>
F/1554-1659/Domain: triple helical domain COLI #status predicted <COLI>
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J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 CKAAKADLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTBF 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1040 SQDD---VNKVSREMQLDGFSFFAIGVADADXS----ELVNIGSKPSERHVFFVDDFD 1090
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831212
collagen alpha 1(XIV) chain precursor, short form - chicken
C,Species: Gallus gallus (chicken)
C,Species: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CPQEDSDIAFLIDGSGSIIPHDFRRMXEFV-STV--MEQLKKSKTLFSLMQYSEEFRIHF
                                                                                                                                                                               AjStatus: preliminary
Anolecula type: mRNA; protein
AjResidues: 1-1747 «GER»
AjCross-references: UNIPROT:P32018
AjExperimental source: embryo skin
AjNote: sequence inconsistent with the nucleotide translation
AjNote: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
R;Trueb, J.; Trueb, B. B.
Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
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                                                                                                             A; Reference number: A45974; MUID:93280195; PMID:8505337
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Best Local Similarity 31.8%; Pred. No. 7.6e-09;
Matches 57; Conservative 28; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March 1992 A; Reference number: $30085 A; Accession: $30085
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Residues: 1472-1659 <GOR1>
Accession: S20833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1472-1660 <APT>
                                                                                                                                                     A;Accession: A45974
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N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952/2; 1041/1; 1146/1;
                                                                     Superfamily: cartilage matrix protein; BGF homology; von Willebrand factor type A repe; Keywords: glycoprotein; homotrimer; 1-22/Domain: signal sequence #status predicted <SIG>; 23-496/Product: cartilage matrix protein #status predicted <WAT>; 23-206/Domain: von Willebrand factor type A repeat homology <VWAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 NNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 HFTFKEFQNNPNPRSLVKPITQ---LLGRTHTATGIRKVVRELFNITNGAR---KNAFKI 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T20G5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
C;Accession: S42373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTL--FSLMQYSEEFRIHFTFKEFQ
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                                                                                                                                                                                                                                             F;27-262/Domain: EGF homology <EGF> F;77-362/Domain: Willebrand factor type A repeat homology <VWA2> F;75.344/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952
F;512-679/Domain: Von Willebrand factor type A repeat homology <VWAl>
F;554-799/Domain: fibronectin type II repeat homology <VRI>
F;154-194/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 215; DB 2; Length 496; 29.9%; Pred. No. 2.5e-11; tive 38; Mismatches 68; Indels
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A; Residues: 1-3051 <SMI>A; Residues: 1-3051 <SMI>A; Cross-references: EMBL: Z30423; NID: g458479; PID: g458485
   A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, March 1994 A;Reference number: 842368 A;Accession: 842373
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rwhulb-c copy 144 320.rpr

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Gaps

< VWA2 >

1095

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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S2254; S28811
C;Accession: A40020; A34485; B344864; B.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obare S;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obare J; Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule windus region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Reference number: A40020; MUID:92011862; PMID:1918137
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A;Molecule type: mRNA
A;Residues: 1.3124 «YAMA
A;Residues: 1.3124 «YAMA
A;Cross-references: UNIPROT: P13944; GB:D00824; NID:G222810; PIDN:BAA00701.1; PID:G222811
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
B;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type IN
A;Reference number: A34485; MUID:90062079; PMID:2584192
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A;Note: this sequence has been revised in reference A34485
K;Noch, M.; Bernasconi, C.; Chiquet, M.
Bur. J. Blochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A;Reference number: S23814; MUID:92362621; PMID:1323460
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A; Redordon, M. K.; Gerecke, D. R.; Olsen, B. R.
B; Gordon, M. K.; Gerecke, D. R.; Olsen, B. R.
A; Title: Type XII collagen: distinct extracellular matrix component discovered by A; Reference number: A28037; MUD:87317590; PMID:3476925
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 2960-2976, F', 2978-3074, AG', AGOR3>
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Modiccule type: mRNA
A;Residues: 2456-2758, A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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        F;352-433/Domain: fibronectin type III repeat homology <FN3B> 4742-525/Domain: fibronectin type III repeat homology <FN3C> F;534-614/Domain: fibronectin type III repeat homology <FN3D> F;623-707/Domain: fibronectin type III repeat homology <FN3D> F;741-823/Domain: fibronectin type III repeat homology <FN3E> F;741-823/Domain: fibronectin type III repeat homology <FN3F> F;322-914/Domain: fibronectin type III repeat homology <FN3F> F;922-1009/Domain: fibronectin type III repeat homology <FN3G> F;1040-1205/Domain: won Willebrand factor type A repeat homology
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    chicken

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A; Residues: 'X, 1333, 'Q', 1335-1347;191
R; Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                             31.8%;
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nes 57; Conservative
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A; Residues: 1-1857 «WAES
A; Cross-references: EMBL:X70792; NID:g288874; PIDN:CAAS0063.1; PID:g288875
A; Cross-references: EMBL:X70792; NID:g288874; PIDN:CAAS0063.1; PID:g288875
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C; Genetics:
C; Genetics:
A; Genetics:
C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
F; 29-1805 / Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F; 29-110, Domain: fibronectin type III repeat homology <FN3B>
F; 352-433 / Domain: fibronectin type III repeat homology <FN3B>
F; 442-552 / Domain: fibronectin type III repeat homology <FN3B>
F; 441-823 / Domain: fibronectin type III repeat homology <FN3B>
F; 441-823 / Domain: fibronectin type III repeat homology <FN3G>
F; 741-823 / Domain: fibronectin type III repeat homology <FN3G>
F; 832-914 / Domain: fibronectin type III repeat homology <FN3G>
F; 822-1009 / Domain: fibronectin type III repeat homology <FN3G>
F; 822-1009 / Domain: fibronectin type III repeat homology <FN3G>
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F; 822-1009 / Domain: fibronectin type III repeat homology <FN3G>
F; 822-1009 / Domain: von Willebrand factor type A repeat homology <FN3G>
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A, Residues: 1-1888 <TRU>
A, Cross-references: UNIPROT: P32018; EMBL: X70793; NID: 9288872; PIDN: CAA50064.1; PID: 92888
R, Waelchi, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Blochem. 212, 483-490, 1993
Eur. J. Blochem. 212, 483-490, 1993
A, Title: Complete primary structure of chicken collagen XIV.
A, Reference number: $31211; MUID: 93185668; PMID: 8444186
A, Accession: §31211
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F:29-188B/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F:29-110/Domain: fibronectin type III repeat homology <FN3A>
[F:29-10/Domain: von Willebrand factor type A repeat homology <VWAI>
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: 878476; S31211
R;Trueb, B.
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                                                     B.; Winterhalter, K.H.; Trueb,
                                                                                                                                                                                                                                                            Status: nucleic acid sequence not shown; translation not shown
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C; Accession: S31212
R; Waalchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
R; Waalchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
Bur. J. Biochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211; MUID:93185668; PMID:8444186
A; Accession: S31212
A; Status; nucleic acid sequence not shown; translation not s
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Pred. No. 8.2e-09
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A;Cross-references: EMBL:X70793
C;Genetics:
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31.8%;
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Jurrons: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
Jurrons: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
Jurrons: 2845/2; 2863/3; 2887/3; 2815/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 2845/2; 284
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;630-711/Domain: fibronectin type III repeat homology «FN3C>
;721-802/Domain: fibronectin type III repeat homology «FN3D>
;812-895/Domain: fibronectin type III repeat homology «FN3E>
;905-986/Domain: fibronectin type III repeat homology «FN3E>
;995-0076/Domain: fibronectin type III repeat homology «FN3F>
;1086-1169/Domain: fibronectin type III repeat homology «FN3F>
;1097-1361/Domain: von Willebrand factor type A repeat homology «FN3H>
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                                                                                                                                                                                                                                               Trueb, J.; Trueb, B.
Cochim. Biophys. Acta 1171, 97-98, 1992
Title: The two splice variants of collagen XII share a'common 5'
Reference number: 828811; MUID:93042014; PMID:1420368
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Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
Cross-references: BMBL:X67327
                                                                                                             Molecule type: protein
Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
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C;Species: Homo sapiens (man)
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C;Accession: A45226
R;Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
A;Accession: A45226
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ntegrin alpha-1 chain - human (fragment)
Species: Homo sapiens (man)
Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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Job time : 6.12706 secs
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       GenCore version (c) 1993 - 2005
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BAD21383
ITAX MOUSE
Q6PG66
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MEDLINE=88315033; PubMed=2457584;
MCDLINE=88315033; PubMed=2457584;
MCDLINE=88315033; PubMed=2457584;
MCDLINE=8831503; PubMed=T.A.;
The human leukcorte adheaion glycoprotein Mac-1 (complement receptor Type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
J. Biol. Chem. 263:12403-12411(1988).
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MEDLINE=88190151; PubMed=2833753;
Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
Arnaout ar Cloning of the alpha subunit of human and guines pig
leukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLINE=88557215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=93123748; PubMed=8419480; Righth T.F., Tenen D.G.; Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.; Structural analysis of the CD11b gene and phylogenetic analysis of "Structural analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-89098893; PubMed-2563162;
Hicketein D.D., Hickey M.J., Ozole J., Baker D.M., Back A.L.,
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                                                                Q95LI2
CAMA MOUSE
Q80VNS
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CAMA_HUMAN
Q8VHĪ5
               Q8HY41
CAMA CHICK
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NCBI_TaxID=9606;
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PDB; 1BHO; X-ray; 1/2=-
PDB; 1BHO; X-ray; 1/2=-
PDB; 1DN; X-ray; 0=140-331.
PDB; 1UDN; X-ray; 0=143-331.
PDB; 1UM; X-ray; 0=143-331.
PDB; 1MIX; X-ray; 0=143-337.
PDB; 1MY; X-ray; A=144-337.
PDB; 1MS; X-ray; A=140-335.
PDB; 1NA5; X-ray; A=140-335.
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AAA59903.1;
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                                                                                                                                                                                                                                                                        EMBL, J04145; PEMBL, S52227; PEMBL, S52153; PEMBL, S52154; PEMBL, S52155; PEMBL, S52155; PEMBL, S52164; PEMBL, S52164; PEMBL, S52169; PEMBL, S52169; PEMBL, S52169; PEMBL, S52180; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52181; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, S52189; PEMBL, 
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PDB; 1A8X; Mc
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EMBL;
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MEDLINE-98226734; PubMed-9560195;

A Oxvig C., Springer T.A.;

Springer T.A.;

Bubunits and a calcium binding site on its lower surface.";

subunits and a calcium binding site on its lower surface.";

Experimental support for a beta-propeller domain in integrin alpha-Mobeta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAMI. It recognizes Pl and P2 peptides of fibrinogen gamma chain.

C -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M associates with beta-2.

C -1- SUBCELLULAR LOCATION: Type I membrane protein.

--- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 WPFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE OF 17-31.
MEDLINE=87076671; PubMed=3539202;
Pierce M.W., Remold-O'Donnell B., Todd R.F. III, Arnaout M.A.;
Pierce M.W., Remold-O'Donnell B.
"N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa.";
Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95171458; PubMed=7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
Crrystal structure of the A domain from the alpha subunit of integrin
"Crrystal structure" of the A domain from the alpha subunit of integrin (Crrystal CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) UF 148-353.
MEDLINE=96363671; PubMed=8747460;
Lee J.O., Bankeron L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=9832595; PubMed=9687375; Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchher V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H., "Cation binding to the integrin CD11b I domain and activation model
                                          SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulared expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                                                                                                                                                  MEDLINE=92144986; PubMed=1346576;
Pabll H.L., Roemarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
  Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structure 3:1333-1340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assessment.";
Structure 6:923-935(1998).
                                                                                                                                                                                                                                   SEQUENCE OF 1-9 FROM N.A. TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80:631-638(1995).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50234; VWPA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0008305; C:integrin complex; TAM.
GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00185; Integrin_alpha; 1.
PRINTS; PR00453; WRAPADOMAIN.
SMART; SM00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
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Name=Itgam;
                          ITAM MOUSE
                                                                                                                                                                                                                    Pytela R.;
                                                                                                        144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVWEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                        BEQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                     204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                      1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                        DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                   264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPFRDHVFQVNNFE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPLGYEDVI PEADRKGVIRYVIGVGDAFNSWKSREELMTIASKPCGDHVFQVNNFE 186
                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                       Score 903; DB 1; Length 1152; Pred. No. 7.4e-67;
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                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920 AA; 102440 MW; E96CC51E350DD5AC CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
              Integrin alpha-M.
                                                                                                                                                                                                                                                                                920 AA
                                                 Pred. No. 7.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOWAIN.
SWART; SM00191; Int_alpha; 4.
SWART; SM00327; VWA; 1.
PROSITE; PSS0224; VWFA; 1.
Cell adhesion; Integrin; Transmembrane.
NON TER.
                                                                                                                                                                                                                                                                                                       Created)
                                    97.9%;
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Matches 141; Conservative
                                                 Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
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 16
1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                           CD11b (Fragment)
                                                                                                                                                                                                                                                                                                       01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                        Name=CD11b;
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                                     Query Match
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SIGNAL
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REQUENCE FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

RAIN=C57BL/6J; TISSUE=Spinal cord;

RAIN=C57BL/6J; TISSUE=Spinal cord;

RA Okazaki Y., Furuno M., Sauto R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Fletcher C., Hume D.A., Quackenbush J.,

RA Gassterland T., Gariboldi M., Glssi C., Godzik A., Gough J.,

RA Gassterland T., Gariboldi M., Glssi C., Godzik A., Gough J.,

RA Gassterland T., Sarabidi M., Marchiomi L., McKenzie L., Miki H.,

RA Kanaj H., Kawaju H., Kawasawa Y., Kedzierski R.M., King B.L.,

RONGAGAYA A., Kurochkin I.V., Lee Y., Lenhard B., Lyons B.A.,

RA Gasterland T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.,

RA Petrovsky N., Pillai R., Pontius J.U., McKenzie L., Miki H.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultana R., Takenaka Y., Taylor M.S., Taesdale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Sultana R., Takenaka Y., Zummer A., Carninci P., Hayatsu N.,

RA Sultana R., Habhizume W., Imotani A., Carninci P., Hayatsu N.,

RA Savolan M., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hara A., Hashizume W., Imotani M., Rasawa M., Sakazume N., Sato K.,

RA Hara A., Habhizume W., Imotani V., Ishiayar K., Shinagawa A.,

Vasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.,

RA Hara A., Hayashizaki Y.
               POSSES, QBCA73;
01-NOV-1988 (Rel. 09, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                     "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willehrand factor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesive interactions of monocytes, macrophages and granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE=Spleen;
MEDLINE=86287312; PubMed=2942940;
Sastre i., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
"A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648 (1986).
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Springer T.A., Teplow D.B., Dreyer W.J.; "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Nature 314:540-542 (1985).
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  1153 AA.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=88312584; PubMed=3044779;
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MEDLINE=85188276; PubMed=3887182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 11-45 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 7:1371-1378(1988).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:563-573(2002)
                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                         NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Willebrand factor
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as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes Pl and P2 peptides of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in mast call development and in immune complex-mediated glomerulonephritis. Mice expressing a null mutation of the alpha-M subunit gene demonstrate increase in neutrophil accumulation, in response to a impaired degranulation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WNFA; 1.
Alternative splicing; Call adhesion;
Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                 ISOId=P05555-2; Sequence=VSP 010473;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                   obesity.
-!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07640; CAA30479.1; -.

EMBL; MA039444; BAC30350.1; -.

EMBL; MA039444; BAC30350.1; -.

EMBL; MA039444; BAC30350.1; -.

EMBL; MA039444; BAC30551.

HSSP; P11215; 1BHO.

MGD; MGI:96607; Itgam.

GG; GG:0007155; P:cell adhesion; IMP.

GG; GG:0007155; P:cell adhesion; IMP.

GG; GG:0007155; P:cell adhesion; IMP.

GG; GG:0007155; P:cell adhesion; IMP.

GG; GG:0007155; P:cell adhesion; IMP.

TherPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF.A.

Pfam; PF00357; Integrin_alpha; 1.

Pfam; PF00357; Integrin_alpha; 1.

Pfam; PF00357; Integrin_alpha; 1.
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Extracellular (Potential).
Potential.
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                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                    IsoId=P05555-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
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SIGNAL 1
CHAIN 17 1153
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                                                                                                                                                                                                                                                                                                                     Name=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fathallah D.M. Sr., Zerria K. Jr.; Sathallah D.M. Sr., Zerria K. Jr.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
-- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; --
HNSSP; PIL155; HBM.
GO: 00008105; C:integrin complex; IEA.
GO: 00008105; P:cell-matrix adhesion; IEA.
                                                                                                                                      (Potential)
(Potential)
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                                                                                                                                                                                                                                                                                                                        127480 MW; 178DB988AECB0343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit.
                                                                                                                                                                                                                                                                                Missing (in isoform
                                                                                                                                                                                                                                                                                                                                           75.1%; Score 692; DB 1; 77.3%; Pred. No. 3.6e-49; ive 18; Mismatches 22;
                                                        By similarity.
By similarity.
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V -> G (in Ref.
                            Potential.
Potential.
GFFKR motif.
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N-linked
FG-GAP 6.
FG-GAP 7.
                  Potential
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683
 683 68
1153 AA;
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PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWPA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
1 19 Potential.
                                                                                                                                                                                                                                                   Integrin alpha-D.
Extracellular (Potential)
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Cytoplasmic (Potential)
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N-linked (GloNA
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Potential
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
                                             InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF00185; PG-GAP; 3.
Pfam; PF00185; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00191; Int alpha; 5.
SWART; SW00327; VWA; Integrin_alpha; 5.
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FG-GAP 2.
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                       EMBL; AF021334; AAF21241.1; -. HSSP; P11215; 1BHQ.
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"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, a novel beta 2 integrin.";

"Cloning of rat alpha D, beta-2 is a receptor for ICAM3 and ACAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloddborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similativy).

"C -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

"C -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

"I - DOMAIN: The integrin I-domain (insert) is a vwFA domain. Integrins with I-domains do not undergo procease cleavage.

"I - SIMILARITY: Contains I VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                          1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                       DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR0000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfam; PF001839; FG-GAP; 2.
Pfam; PF001839; FG-GAP; 2.
Pfam; PF00092; VWA; 1.
PFam; PR00092; VWA; 1.
PRINTS; PR00191; Int_alpha; 5.
RNART; SM00191; Int_alpha; 5.
RNART; SM00191; Int_alpha; 5.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
PR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
RPR08ITE; PS00242; INTEGRIN ALPHA; 1.
                                                                                                                                                                                                                 Score 669; DB 2; Length 1151;
Pred. No. 3e-47;
11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
                                                                                                                                                                                                       72.6%; Sco...
y 73.9%; Pred. No. 3e...
'''n 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin alpha-D precursor
Name=Itgad;
                                                                                                                                                                                                                                                  Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                   Best Local Similarity
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205
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                                                                                                                                                                                                                                                                                                           146 CPRQEMDIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFT
                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 DPLEYSDVIPAADKAGIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGNF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNF 175
                                      (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential)
                                                                                                                                                                                                    59.7%; Score 550; DB 1; Length 1161; 60.6%; Pred. No. 2.8e-37; tive 27; Mismatches 42; Indels (
                                                                                                                                         1045 1045 N-linked (GlcNAc. . .) (Pote
1161 AA; 126600 MW; 2258491A984A705E CRC64;
                                                                                                 (GlcNAc. . .)
                                                                                (GlcNAc. . .)
                   (GlcNAc.
                                                           (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1162 AA
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ID TITAD HUMAN STANDARD,
AC Q13349; Q15575; Q15576;
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16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2)

(Rel. 40, Created) (Rel. 40, Last seq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE=96257236; PubMed=8666289; Wong D.A., Davis B.M., LeBeau M., Springer T.A.; "Ichning and ciromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit."; Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin
gene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Stautcon D.E., Bochner B.S., alphabbata2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
                                                                                                                                                                                                                                                                                                                                                           Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.; "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                   MEDLINE=96111956; PubMed=8777714;
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                                                                                                          Name=ITGAD;
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MIM, 602453; ...

R MIM, 602453; ...

R GO; GO:0008305; C:integrin complex; TAS.

R GO; GO:0016337; P:cell-cell adhesion; NAS.

R GO; GO:0001631; P:cell-matrix adhesion; NAS.

R GO; GO:0006955; P:immune response; NAS.

R GO; GO:0006955; P:immune response; NAS.

R InterPro; IPR002035; VWF, A.

R InterPro; IRR002035; VWF, A.

R Pfam; PF01839; FRC1484; I.

R Pfam; PF00397; Integrin_alpha; I.

R Pfam; PR00929; VWA, I.

R RINTS; PR00453; VWFADOMAIN.

R RART; SR00121; Int alpha; I.

R RART; SR00121; Int alpha; I.

R ROSITE; PS0242; INTEGRIN ALPHA; I.

R ROSITE; PS0244; VWFA, I.

R ROSITE; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Extracellular (Potential).
Potential.
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GHPW -> ATTP (in Ref. 2).
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60.0%; Pred. No. 7.5e-37;
ive 29; Mismatches 41;
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or send an email to license@isb-sib.ch)
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FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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                                         EMBL, U37028, AAB38547.1; -.
EMBL, U40274, AAB60634.1; -.
EMBL, U40275, AAB60635.1; -.
EMBL, U40276, AAB60637.1; -.
EMBL, U40277, AAB60637.1; -.
EMBL, U40279, AAB60638.1; -.
EMBL, U40279, AAB60638.1; -.
EMBL, U40279, AAB60638.1; -.
EMBL, U40279, AAB60638.1; -.
EMBL, U40279, AAB60638.1; -.
EMBL, U40279, AAB60638.1; -.
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SIGNAL 17
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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  EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                      KVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFR 149
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CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                        264 DPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELNTISSAPPQDHVFKVDNF 318
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P20702; Q8IVA6;
01-FBE-1991 (Rel. 17, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95 alpha chain) (Leukocyte adhesion receptor p150,95)
Name=ITGAX; Synonyan=CD11C;
                                                                                                                                                                DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar Kyoto;
Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,
Julier C., Masuda J., Yamori Y., Nara Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59801; AAB03226.1; -.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 533; DB 2; Length 205; Pred. No. 1.1e-36;
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205 AA; 22922 MW; C8C2D9395008DA36 CRC64;
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74.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Itgam;
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DT 01-CTD
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MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A.S., Schein J.B., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABABS: NAWE=PROW; NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
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                                    MEDLINE-88166665; PubMed-3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
Corbi A.L., miller b.J., O'Connor K., Larson R.S., Springer T.A.;
Corbi Joning and complete primary structure of the alpha subunit
leukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      important in monocyte adhesion and chemotaxis.
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
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J. Biol. Chem. 265:12750-12751(1990).
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kikuno R., Ohara O., Koga H.;

Brediction of the Coding Sequences of Mouse Homologues of FLJ Genes:

The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNAs Sampled from Size-Fractionated Libraries.";

DNA Res. 11:167-180(2004).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   D -> L (in Ref. 1).
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SEK -> TPHYPQDNV (in Ref. 4).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Name=mFLJ00114;
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G -> A (in Ref. 2).
E -> K (in Ref. 2).
                                       EMBL, M81695, AAA59180.1; -. EMBL, M29165; -; NOT ANNOTATED CDS. EMBL, M29482; AAA51620.1; AAT SEQ. EMBL, M29482; AAA51620.1; JOINED. EMBL, M29483; AAA51620.1; JOINED. EMBL, M29484; AAA51620.1; JOINED. EMBL, M29486; AAA51620.1; JOINED. EMBL, M29486; AAA51620.1; JOINED. EMBL, M29486; AAA51620.1; JOINED. EMBL, M29486; AAA51620.1; JOINED. EMBL, BC038237; AAH38237.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                           225 NFISTSSPLELLDSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVITDGRKQG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 CPKQDQDIVFLIDGSGSISSTDFEKMLDFVKAVMSQLQRPSTRFSLMQFSDYFRVHFTFN 224
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C -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

C -!- SIMILARITY: Belongs to the integrin alpha chain family.

EMBL, AK1311313 BAD21383.1, -.

R GO; GO:0009897; C:external is ede of plasma membrane; IDA.

InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR002035; VWF.A.

R Pfam; PF0040357; Integrin_alpha; 1.

R Pfam; PF0040357; Integrin_alpha; 1.

R Pfam; PF0040357; Integrin_alpha; 1.

R PRINTS; PR00453; VWA7 1.

R RRINTS; RR00453; VWPADOMAIN.

R SMART; SW00191; Int alpha; 5.

SMART; SW00191; Int alpha; 5.
                                                                                                                                                                                                                                                                                                                     1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;

"Prediction of the Coding Sequences of Mouse Homologues of FLJ Gente:
The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNÄs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AK131133; BAD21383.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                285 DNLSYDSVIPMAEAASIIRYAIGVGKAFYNEHSKOELKAIASMPSHEYVFSVENFD 340
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                               52.4%; Score 483; DB 2; Length 1188; 52.8%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                         53; Indels
                                                                                                                                                                                                                                    SEQUENCE 1188 AA; 131248 MW; B8D93107BDBB4178 CRC64;
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                           PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
PROSITE; PS50234; VWPA; 1.
Cell adhesion; Integrin; Transmembrane.
                                                                                                                                                                                                                                                                                         30; Mismatches
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"Isolation of genes selectively expressed by dendritic cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DbBJ databases.
Isolation of genes selectively expressed by dendritic cells.";
Committed (DEC-1999) to the EMBL/GenBank/DbBJ databases.
Interaction interaction alpha=x/beta=2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis (By similarity).

Committed in a light and a beta subunit. Alpha=X associates with beta=2 (By similarity).

Committed in a light and a beta subunit. Alpha=X associates with beta=2 (By similarity).

Committed in integrin I chamin (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

Committed in a VMFA domain (insert) is a VMFA domain family.

Committed in a VMFA domain.
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285 DNLSYDSVIPWAEAASIIRYAIGVGKAFYNEHSKQELKAIASMPSHEYVPSVENFD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Dendritic cell;
Huang X., Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll D.,
                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
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GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR00313; VWF. A.
Pfam; PF01819; FG-GAP; 3.
Pfam; PF00052; Integrin_alpha; 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00127; VWA; 1.
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Integrin alpha-X.
Extracellular (Potential).
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Integrin alpha X.
Mus musculus (Mouse)
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AAH57200;
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MEDINE-2238257; PubMed=1247793;

MEDINE-2238257; PubMed=1247793;

MEDINE-2238257; PubMed=1247793;

MAGNER R.D., Colling F.S., Wagner L.H., Derge J.G.,

MARCHIL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MARCHIL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MARCHIL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MARCHIL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MARCHIL M.J., Uddin T.B., Toshiyui S., Carninci P., Prange C.,

MARCHIL M.J., Uddin T.B., Toshiyui S., Carninci P., Mullahy S.J.,

MARCHIL M.J., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

MARCHIL M., Sodergren B.J., Lu X., Galbe R.A.,

MARCHIL M., Sodergren B.J., Lu X., Galbe R.A.,

MARCHIL M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MARCHIL M., TOUCHMAN J.W., Green B.D., Dickson M.C.,

MARCHILL M., TOUCHMAN J.W., Schwutz J., Myers R.M., Butterfield Y.S.,

MARCHILL M., Madan J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                     C616412033C219A6 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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les 93; Conservative
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STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

MEDLINE=21388257; PubMed=12477932;

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MEDLINE=21388257; PubMed=1257;

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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=129; TISSUE-Mammary tumor. Brcal-/fl;
Strausberg R.;
Subminced (Aug. 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057200, AAH57200.1;
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
InterPro; IPR002035; VWF.A.
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
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-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

EMBL; AR133079; AAD30063.1; JOINED.

EMBL; AR133077; AAD30063.1; JOINED.

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EMBL; AR133078; AAD30063.1; JOINED.

EMBL; AR133087; AAD30063.1; JOINED.

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EMBL; AR133087; AAD30063.1; JOINED.

EMBL; AR133087; AAD30063.1; JOINED.

EMBL; AR133087; CILLEGTIN complex; IEA.

InterPro; IRR000413; Integrin complex; IEA.

InterPro; IRR002035; VWP.A.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                44.3%; Score 408; DB 2; Length 304; 53.3%; Pred. No. 5.1e-26; wative 25; Mismatches 43; Indels
[2]
SEQUENCE FROM N.A.
STRAIN-129; TISSUE-Mammary tumor. Brcal-/fl;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO57200; AAH57200.1; -.
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Last annotation update)
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Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM0191; Int_alpha; 4.
SWART; SM00327; VWA; 1.
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Matches 80; Conservative
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Name=Itgae;
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                                                                                                                                                                                                                                                                                                                                                   3 QEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL--KKSKTLFSLMQYSBEFRIHFTFK 60
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STRANTE-STBL/GJ TISSUE-Aorta and vein;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/60; TISSUE-Aorta and vein;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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178 EDGTEIAIVLDGSGSIEPSDFQKAKNFISTWMRNFYEKCFECNFALVQYGAVIQTEFDLQ
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530055010 product:integrin, alpha E,
epithelial-associated, full insert sequence.
                                                                                                                                                                                                                 Length 895;
                                                                                                                                                                                                                                                                              66; Indels
                                                                                                                                            895 AA; 98265 MW; BE6EA14A754ADA1E CRC64;
                                                                                                                                                                                                             34.9%; Score 322; DB 2; 38.3%; Pred. No. 2.7e-18; iive 40; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Aorta and vein; MBDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Aorta and.vein;
MEDLINE=20530913; PubMed=11076861;
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=21085660; PubMed=11217851;
PROSITE; PS50234; VWPA; 1.
Cell adhesion; Integrin; Transmembrane.
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NON_TER 895 895
SEQÜENCE 895 AA; 98265 WW; BE6EA14A
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-!- SUBMILARITY: Belongs to the integrin alpha chain family.

R EMBL, AKO40983; BAC30769.1; -.
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               Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Samamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishiwawa T., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., "RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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MGD; MGI:1298305; C:integrin complex; IEA.

GO; GO:0007160; P:cell-matrix adhesion; IEA.

GO; GO:0007229; P:integrin.mediated signaling pathway; IEA.

InterPro; IPR000413; Integrin.alpha.

InterPro; PF01839; PG24P; 3.

Pfam; PF01839; PG4P; 3.
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Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1038 AA; 114722 MW; 2EBIDE7660795587 CRC64;
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Job time : 38.0546 secs
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SWART; SM00327; VWA; 1.
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Human, integrin alpha subunit; A domain, CD11b; integrin beta subunit; Alike domain; inflammacory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a high affinity integrin polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human integrin alpha subunit CD11b deletion variant A domain #2.
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13-MAR-2001; 2001US-00805354.
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call or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the Collb alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or C decermining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing shelteral muscle injury, for treating disorders caused by ischaemia.

The purify variant integrin polypeptide ligands and as bait proteins in the public or three-hybrid assays. This sequence represents a human integrin alpha subunit CD11b deletion variant. A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76847
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Sequence 177 AA;

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BFONNPNPRSLVKPITOLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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AAY21991 standard; protein; 187 AA AAY21991; RESULT 2 AAY21991 CENTRAL SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVIC

13-SEP-1999 (first entry)

Human complement factor MAC-1 vWF domain sequence.

Factor B analogue; modified; complement activity; complement factor B; short consensus repeat domain; von Willebrand Factor domain; human; C2; CR3; autoimmune response; tissue damage; lupus erythematosus; therapy; rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1; myocardial infarction; acute shock lung syndrome; inflammation; vWF.

Homo sapiens

US5928892-A.

27-JUL-1999

96US-00687706. 26-JUL-1996; 94US-00177109. 03-JAN-1994;

(UNIW ) UNIV WASHINGTON

Oglesby TJ, Hourcade DE;

WPI; 1999-429498/36.

Nucleic acids encoding complement protein homologues useful for modulating function of the complement system in the treatment of variety of immune and autoimmune complex mediated syndromes.

Disclosure; Fig 5A-B; 53pp; English

17-JUL-2002; 2002US-0396783P. 17-JUL-2003; 2003WO-US022301.

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complement activity in vitro. The analogue is generated by substituting a short consensus repeat domain (SCR) or a von Willebrand Factor domain (SCR) or a von Willebrand Factor domain as to thuman factor B with a SCR or a vwF from a second protein such as thuman C2 or CR3. The analogues may be used to regulate the complement system involved in immune and autoimmune responses. Complement activity can account for substantial tissue damage in a wide variety of autoimmune (SCR) immune complex mediated syndromes such as lupus erythematosus, inhibition of intervention in these cases. Inhibition of complement may also be favorable in cases that involve tissue damage caused by vascular calso be favorable in cases that involve tissue damage caused by vascular and of the destruction of partially damaged tissue as in contribute to the destruction of partially damaged tissue as in creperfusion injury. In addition, the use of complement system may contribute to the destruction of partially damaged tissue as in creperfusion injury. In addition, the use of complement analogues with conversing a sites of inflammation. Complement inhibition is important in the prevention of xenopalement by cell-associated and soluble inhibitors is useful in protecting the transplant from damage caused by activation of complement. The present sequence represents the vWF domain of human factor MAC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrin alpha subunit; beta; antipsoriatic; thrombolytic; anticoagulant; osteopathic; cytostatic; immunosuppressive; antiinflammatory; europrotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thromboals; cancer; osteoporosis; sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                   The invention relates to a Factor B analogue that exhibits modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 903; DB 2; Length 18
99.4%; Pred. No. 2.9e-93;
ive 0; Mismatches 1; Indels
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Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 187 AA;
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20-DEC-2002; 2002US-00325899.
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                                                            Wohlgemuth J, Fry K,
Rosenberg S;
                                                                                                         WPI; 2004-400724/37.
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07-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                          The invention relates to a novel isolated or recombinant modified integrin protein having extracellular domains of integrin alpha and beta subunits where one of the subunits has one or more mutations, an altered surface feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-cysteine residue to cysteine or extracellular domains of integrin alpha and beta subunits. The polypeptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic, cytosteatic, immunosuppressive, antiinflammatory, neuroprotective and antisickling activities and may be useful for immunotherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple sclerosis. The current sequence is that of the human integrin alpham such an unit precursor protein of the invention.
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                                                                                                                                                     Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 3.7e-92;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP12435 standard; protein; 1152 AA
17-JUL-2002; 2002US-0396790P.
11-SEP-2002; 2002US-0410135P.
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                                             (BLOO-) CENT BLOOD RES INC.
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Best Local Similarity 99.4
Matches 175; Conservative
                                                                          Takagi J;
                                                                                                         2004-122877/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1152 AA;
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                                                                          Springer TA,
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204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
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                                                                                                                                                                                                                                                                          Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, and individual. The method is also useful in assessing the immune status of an individual. The method is also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to diagnosing or monitoring transplant
                                                                                    Morris M;
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99.4%; Pred. No. 3.7e-92;
ive 0; Mismatches 1; Indels
                                                                                Prentice J,
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non-specific defence system; integrin gene superfamily
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/label= signal_peptide
86. .88
/label= putative N-glycosylation site
240. .242
/label= putative N-glycosylation site
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                                                                            Ly N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 65; SEQ ID NO 2444; 1762pp; English.
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(EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                                            Woodward R,
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Matches 175, Conservative
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Modified-site

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Mac-1 alpha subunit is involved in the response to inflammation, i.e. recognition of and migration to sites of inflammation. It also attaches to cellular substrates as part of this function making it useful in visualising endothelial tissue. Mac-1 is a member of the Integrin Gene superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating inflammation and viral infections, and in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 903; DB 2; Length 1153;
Pred. No. 3.7e-92;
0; Mismatches 1; Indels
                                                                                                /label= putative N-glycosylation site 12abel= putative N-glycosylation site 12abel= putative V
                                                                                                                                                                 /label= putative N-glycosylation site 941. 943
                                                                                                                                                                                                                                  Label= putative N-glycosylation site (79. 981
391. .393
/label= putative N-glycosylation site
469. .471
/label= putative v
                                .abel= putative N-glycosylation site (593 . 695 . 1abel= putative ...
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abel= putative N-glycosylation site
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label= putative N-glycosylation site
051. .1053
label= putative N-glycosylation site
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                                                                                                                                                                                                                                                                                                                       label= putative N-glycosylation site
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|abel= putative N-glycosylation |
106. .1134
                                                                            ...abel= putative N-glycosylation 735. .737
                                                                                                                      Label = putative N-glycosylation 181. 1883
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                                                    ....yiation
697. 699
7label= putative N-glycosylation
7label= putative
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Best Local Similarity 99.4%;
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corbi A;
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                                                                                                                                 Modified-site
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This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                                                                                                                                                             Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit;
                 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                       DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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                                                                                                                                                                                                                                                                                                                     Human Beta-integrin CD11b subunit protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 1A-D; 106pp; English.
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                                                                                                                                                                                                                             AAW65090 standard; protein; 1153
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94US-00286889.
94US-00362652.
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                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis
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264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319

Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.

Homo sapiens

Human integrin 1 alpha-M subunit protein.

(first entry)

15-JUL-2002

AAU80252;

AAU80252 standard; protein; 1153

DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFF 176

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Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury sites.
                                                                EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; macrophage infiltration inhibition; alpha_d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adheaion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.
CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or immosupcessive activities. The polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for transmitting an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease, nephritis; human immunodeficiency virus (HIV), myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified integrin-I or integrin I-like domain polypeptide useful as a immunogen to produce antibodies specific to polypeptide, comprises a disulfide bond such that polypeptide is stabilized in a desired
                                                                                                                                                                                                                                                Misc-difference 499. .500
/note= "Encoded by GGG CAG AGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 109-112; 112pp; English.
                                                                                                                                                                                                                                    Location/Qualifiers
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C
                                                                                                                                                                                                                                                                                                                                                                     31-AUG-2001; 2001WO-US027227.
                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000US-0229700P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (BLOO-) CENT BLOOD RES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conformation
                                                                                                                                                                                                                                                                                                                                    07-MAR-2002
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have an integrins. Leu-CAMS, leukointegrins or beta2 subunit: the leukocyte integrins. Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence responsing in a alignment to identify a novel beta2 integrin alpha sequence has approximately 60% identity to the protein sequence has approximately 60% identity to the protein sequence of alpha d. The caberrant alpha d function engory protein sequence of alpha d. The aberrant alpha d function engory inflammation, acute respiratory clatress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclomal antibodies may be used in the inflation of macrophage infiltration at the site of a central nervous system injury. The monoclomal antibodies can also be used to detect and

diagnose Crohn's disease

Sequence 1153 AA;

Example 5; Fig 1; 270pp; English.

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Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-l alpha-M protein subunit used to generate the mutant polypeptides of the invention
                                                                                                                                                                                                                                                                                                EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                  144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta2 integrin, alphaD subunit, CD11c subunit, CD11b subunit; LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis, arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; aucomotor recovery; locomotor damage; locomotor impairment; autonomic dysfunction; sensory dysfunction; spinal cord injury.
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                                                                                                                                                                                                                                                                                                                                            DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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Pred. No. 3.7e-92;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Beta2 integrin alphaCD11b subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG61469 standard; protein; 1153 AA
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                                                                                                                                                         97.9%;
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                                                                                                                                                                                      Matches 175; Conservative
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                                                                                                                                                                         Local Similarity
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                                                                                                                           Sequence 1153 AA;
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The invention relates to promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand

Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.

Example 5; Page 191-194; 270pp; English.

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selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphaD cobns and proteins, for use in raising the antibodies. Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the
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integrin related immunological disorder; rheumatoid arthritis; ischaemia;
reperfusion; hypovolemic shock; infarction; cerebral shock;
viral infection; cancer; gene therapy; vaccine;
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99.4%; Pred. No. 3.7e-92;
iive 0; Mismatches 1;
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Matches 175; Conservative
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ADD25615 standard; protein; 1153 AA
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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The invention relates to a binding domain-immunoglobulin fusion protein comprehence a binding domain polypeptide, an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain (FR constant region polypeptide that is fused to the hinge region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human iggli immunoglobulin hinge region polypeptide comprises: a wild-type human iggli immunoglobulin hinge region polypeptide. The mutated human iggli immunoglobulin hinge region polypeptide comprises: a wild-type human iggli immunoglobulin hinge region polypeptide contains contains 2 cysteine residues, where the first cysteine is not mutated; human iggli immunoglobulin hinge region polypeptide contains of mutated human iggli immunoglobulin hinge region polypeptide contains contains and a mutated human iggli immunoglobulin hinge region polypeptide contains or cysteine residues; where the first cysteine residues, where the first cysteine residues and a mutated human iggli immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein is useful for treating a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein equanced at an isolated with a recombinant and condition or an abected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumoglobulin fusion protein-associa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                   New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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99.4%; Pred. No. 3.7e-92;
ive 0; Mismatches 1; Indels
                                                                                                                                                                      Disclosure; SEQ ID NO 176; 157pp; English
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                                                                                                domain proteins, wherein the alterations to the protein curegin inserted (1) proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally bissed to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins and nucleic acids are useful for treating. Preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatoid arthritis). The variant integrin I domain proteins and nucleic acids can also be used for treating, reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for alpha subunit of integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; famunoglobulin heavy chain; CH2 constant region; CH3 constant region, IgG1, antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent conflictor; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                    invention comprises structurally biased variant integrin inserted (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPQEDSDIAFLIDGSGSIIPHDFRRMKBFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.9%; Score 903; DB 5; Length 1153; 99.4%; Pred. No. 3.7e-92; ive 0; Mismatches 1; Indels
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                           Example 1; Fig 1F; 90pp; English.
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AAU76865;

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Claim 19; Page; 55pp; English.
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11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                                                                               31-JUL-2001; 2001WO-US023957
                                                                                                                                                     Arnaout AM, Li R, Xiong J;
    21-MAY-2002 (first entry)
                                                                                                                                           (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                              WPI; 2002-188687/24
                                                                               Misc-difference 177
                                                                     Misc-difference 17
                                                                                                                                                                                                                                                                                        Sequence 177 AA;
                                                                                            WO200209737-A1
                                                   Homo sapiens,
                                                                                                      07-FEB-2002,
                                                        Synthetic.
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Jest Local Similarity ....

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Local Similarity

Location/Qualifiers

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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or for a residue 313 and A at residue 320 have been replaced by C, or for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, immune complexes, restenses and parasitic diseases, reperfusion injury, immune complexes, restenses and parasitic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-like domain; inflammactory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
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                                 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFEC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Gly, Ala
/note= "Wild-type Ile substituted by Gly or Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Human integrin alpha subunit CD11b variant A domain.
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                                                                                                                                                                                                                            AAU76856 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                        AAU76856;
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                                                                                                                 Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit; A-like domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
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                                                     Human integrin alpha subunit CD11b deletion variant A domain #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Wild-type Phe substituted by Cys"
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integrin alpha subunit CD11b A domain
                                      Sequence 191 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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Best Local &
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                                                                                                  EFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                   restenosis;
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                                                                                                               CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                               CPQEDSDIAFLIDGSGS1IPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                    DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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    188
    /note= "This region is specifically claimed"

                        Indels
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            4e-92;
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                       Mismatches
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97.78; Pic.
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11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                                (first entry)
         Best Local Similarity 97.7
Matches 172; Conservative
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The present invention relates to generating a specific binding partner to a peptide, encoded by a genomic DNA fragment or an expressed sequence tag (EST). A nucleic acid molecule encoding a fusion protein is expressed in a host cell to allow the formation of inclusion bodies comprising the fusion protein, the inclusion bodies are isolated and a specific binding partner is generated. The specific binding partners generated are useful for identifying and characterizing naturally occurring proteins e.g. as immunoglobulins or fragments in immunoassays
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                                                                                                                                                                                                                                                   61 EPQNNPNPRSLVKPITQLIGRTHIATGIRKVVRELFNITNGARKNAFKLLVVLTDGEKFG 120
                                                                                                                                                                                                                 61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                            1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generating specific binding partners to (poly)peptides encoded by g
DNA fragments, involves forming inclusion bodies by expressing the
(poly)peptide as part of fusion proteins.
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  Length 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of human CR-3 alpha chain and His tag.
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Pred. No. 1.4e-89;
                                                     2; Indels
                                                                                                       1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKS
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     DB 5;
Score 893; DB 5;
Pred. No. 4e-92;
2; Mismatches
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Search completed: January 13, 2005, 15:12:33 Job time : 34.0928 secs

Sequence 9, Appli Sequence 48, Appli Sequence 5, Appli Sequence 11, Appli Sequence 111, Appli Sequence 101, Appli Sequence 101, Appli Sequence 37, Appli Sequence 55, Appli Sequence 55, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 99, Appli Sequence 99, Appli Sequence 65, Appli Sequence 65, Appli Sequence 67, Appli Sequence 67, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence:

Run on:

Searched:

Database

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Sequence 1, Application US/09805354

Sequence 1, Application No. US20030078375A1

GENERAL INFORMATION:

APPLICANT: Armaout, M. Amin

APPLICANT: Atmout, M. Amin

APPLICANT: Almout, M. Amin

APPLICANT: Xiong, Jian-Ping

TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF

TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/805,354

CURRENT FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-07-31

PRIOR SPELICATION NUMBER: US 60/221,950

SPRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PRELEGE for Windows Version 4.0

FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SEQ ID NOS: 20

SEQ ID NO 1.
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Pred. No. 6.2e-89;
0; Mismatches 1; Indels
5 US-10-346-863-37

6 US-10-346-863-42

5 US-10-346-863-48

10 US-09-902-481A-5

10 US-09-902-481A-3

10 US-09-902-481A-3

10 US-09-350-259-101

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US-09-350-259-4
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Matches 175; Conservative (
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; ORGANISM: Homo sapiens
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                                                                                              January 13, 2005, 15:13:36; Search time 29.2475 Seconds (without alignments) 2186.449 Million cell updatés/sec
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1 CPQEDSDIAFLIDGSGSIIP......NTIASKPPRDHVFQÇNNFEC 177
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US-09-902-481A-6

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Best Local Similarity 99.4 Matches 175, Conservative
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ORGANISM: Homo sapiens
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DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                              DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2000-00-04
PRIOR APPLICATION NUMBER: US 60/758,493
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                             Sequence 1, Application US/09758493
; Sequence 1, Application No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2000-01-11
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO.
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Matches 175; Conservative
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Matches 175; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 4, Application US/09945265
; Patent No. US20020123614A1
; GERERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Springer, Motomu
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
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; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED
; TITLE OF INVENTION: UNMBER: US 60/229,700
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR PILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FRASEEQ for Windows Version 4.0
; SEQ ID NO 4.
                                                                                                                                                                                                       61 BFQNNPNPRSLVKPITQLIGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                              1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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Patent No. US20020062008A1
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20020062008A1el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1998-01-08
EARLIER PEPLICATION NUMBER: 09/193,043
EARLIER PILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/13,497
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/36,652
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99.4%; Pred. No. 7.3e-88;
tive 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICAMY: Gallatin, Michael W.
APPLICAMY: Gallatin, Michael W.
APPLICAMY: Gallatin, Michael W.
APPLICAMY: Gallatin, Michael W.
TITLE CAMY: Gallatin, Michael W.
TITLE OF INVENTION: NO. US20030077278Alel Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT PLING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR PLING DATE: 1994-10-05
PRIOR PLING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR PRILING DATE: 1994-12-21
PRIOR PLING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PAECHLIN VOYE: 2.0
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Best Local Similarity 99.4
Matches 175, Conservative
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ORGANISM: Homo sapiens
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| Bublication No. US20030054440A1
| GENERAL INFORMATION:
| APPLICANT: Springer, Timothy
| APPLICANT: Springer, Timothy
| APPLICANT: Shifman, Unlia
| APPLICANT: Shifman, Unlia
| APPLICANT: Shifman, Unlia
| APPLICANT: Mayo, Stephen
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
| FILE REFERENCE: A-70586-1/RFT/RMS/RMK
| CURRENT FILING DATE: 2001-07-07
| PRIOR APPLICATION NUMBER: US 60/216,600
| PRIOR PILING DATE: 2000-07-07
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 1
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            EARLIER FILING DATE: 1997-10-03
                              NUMBER OF SEQ ID NOS: 114
SOFTWARB: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1153
TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: mat_peptide
LOCATION: (17)..()
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US-09-902-481A-1
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US-09-902-481A-1
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US-09-891-943-3
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00786-548001
CURRENT PAPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 69/758,493
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
CHUBBER: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1153
TYPE: PRT
CREANISM: Homo sapiens
US-10-144-259-30
                                                               0; Gaps
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97.9%; Score 903; DB 10; Length 1153; 99.4%; Pred. No. 7.4e-88; tive 0; Mismatches 1; Indels 0
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Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 175; Conservative 0; Mismatches 1;
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; Sequence 3, Application US/09891943

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Sequence 5, Application US/09902481A Publication No. US20030054440A1 GENERAL INFORMATION:
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic US-09-902-481A-5
                                                                                                                                                                                                                                                                                                                                                    US-09-902-481A-5
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EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                             204 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG
                                                                                         121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                                                                                 264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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                                                                                                                                                                                                                                          Publication No. US20030118592A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION:
BINDING DOWAIN-INWUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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Publication No. US20030054440A1
Publication No. US20030054440A1
APPLICANT: Shimaoka, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
CURRENT APPLICATION NUMBER: US/08/902,481A
CURRENT FILING DATE: 2001-07-09
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 99.4<sup>3</sup>
Matches 175; Conservative
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US-10-207-655-176
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US-10-207-655-176
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US-09-902-481A-6
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LENGTH: 1137
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APPLICANT: Shimmacka, Motcomu
APPLICANT: Shimmacka, Motcomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A.70586-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
: SEQ ID NO 5
LENGTH: 1137
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APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimao, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: 12001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR APPLICATION NUMBER: US 60/216,600
NUMBER OF SEQ ID MOS: 7
SOFTWARE: Patentin version 3.1
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Best Local Similarity 95.5%; Pred. No. 2.3e-86;
Matches 168; Conservative 6; Mismatches 2;
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TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-346-863-37
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                                                                                                                                                                                                               Query Match 95.3%; Score 879; DB 10; Best Local Similarity 94.9%; Pred. No. 2.8e-85; Matches 167; Conservative 6; Mismatches 3;
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Pred. No. 3.8e-86;
0; Mismatches 1;
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Publication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GTTERINGE, ALEX
TITLE OF INVERTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT APPLICATION NUMBER: PCT/091
PRIOR FILING DATE: 2003-01-17
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR APPLICATION NUMBER: GB 0025447.4
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
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; Sequence 37, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 171; Conservative
                                                                                 ORGANISM: Artificial sequence
                                                                                                                                    , OTHER INFORMATION: synthetic US-09-902-481A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-10-346-863-17
SEQ ID NO 4
LENGTH: 1137
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LENGTH: 184
                                                           TYPE: PRT
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95.1%; Score 877; DB 16; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 171; Conservative 0; Mismatches 1; Indels
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Pred. No. 3.9e-86;
0; Mismatches 1;
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PRIOR FILING DATE: 2001-01.11

PRIOR FILING DATE: 2001-01.11

PRIOR APPLICATION NUMBER: GB 0100750.9

PRIOR FILING DATE: 2001-01.11

SEQIENT ON SEQIEN NOS: 12

SEQIEN NO 9.
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GUTTERIDGE, ALEX
TILE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 37
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Best Local Similarity 99.4%;
Matches 171; Conservative
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125 YEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176

Search completed: January 13, 2005, 15:39:45 Job time : 30.2475 secs

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61 EFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Patrea L. Pabst STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta STATE: Georgia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 30309-3450

COMPUTER RELABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/17,109A
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabbat, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
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REFERENCE/DOCKET NUMBER: 31,2
US-08-605-672-37
US-08-482-293A-37
US-08-193-363-37
US-09-193-043-37
US-09-180-259-37
US-08-485-618-55
US-08-652-55
US-08-943-353-55
US-08-193-043-55
US-09-193-043-55
US-09-193-043-55
US-09-193-043-55
US-09-193-043-55
US-08-173-497-2
US-08-173-497-2
US-08-173-497-2
US-08-185-618-29
US-08-185-618-29
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-177-109A-61
; Sequence 61, Application US/08177109A
Patent No. 5869615
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 187 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein;
HYPOTHETICAL: NO
US-08-177-109A-61
   linear
   TOPOLOGY:
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Sequence 101, App
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
                                                                                                                           January 13, 2005, 15:07:42; Search time 8.50625 Seconds (without alignments) 1379.959 Million cell updates/sec
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1 CPQEDSDIAFLIDGSGSIIP......NTIASKPPRDHVFQCNNFEC 177
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-187-6134-43

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US-08-186-889-3

US-08-186-889-3

US-08-186-18-3

US-08-186-18-3

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US-09-193-04-3

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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                  RWHU1B-C_COPY_144_320
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                       Copyright
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                                                                                                                                                                                                  Title:
Perfect score:
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GENERAL INFORMATION:
APPLICANT: Arnaou
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                           121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 176
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                                                                                                                                                                                                          Sequence 61, Application US/08687706
Patent No. 5928892
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Alamtic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26-JUL-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION: UNMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-476-062A-43
; Sequence 43, Application US/08476062A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (404) 873-8794
TELEPAK: (404) 873-8795
INPORMATION FOR SEO ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 187 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.4*
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO US-08-687-706-61
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Atlanta
STATE: Georgia
                                                                                                                                                                             RESULT 2
US-08-687-706-61
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
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       CONTROLLING CELLULAR IMMUNE/INFLAMMATORY RESPONSES WITH BETA2 INTEGRINS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1152;
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TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                   COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFRATING SYSTEM: Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-10N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/216,081
FILING DATE: 21-MAR-1994
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 28-JUN-1990
APPLICATION NUMBER: 07/512,573
FILING DATE: 28-JUN-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 903; DB 2;
Pred. No. 1e-91;
0; Mismatches
                                                                                                       ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US96-01314-43; Sequence 43, Application PC/TUS9601314; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.9%;
Best Local Similarity 99.4%;
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1152 amino acids
TITLE OF INVENTION: CONTITLE OF INVENTION: RESENUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESSES: Fish & Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Freeman, John W. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
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144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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                                                                                                                                                                                                                                   264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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                                                                                                                                                                                              121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PCE-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27866/31363
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Patent No. 5437958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                US-08-173-497-3
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PAPLICANT: ARNAOUT, M. AMIN

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FILING DATE: 16-JUN-1993

PRIOR APPLICATION NUMBER: 539,842

FILING DATE: 18-JUN-1990

PRILING DATE: 18-JUN-1990

PRILING DATE: 28-JUN-1990

FILING DATE: 28-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 903; DB 6;
Pred. No. 1e-91;
0; Mismatches
                                                                                                  COUNTRY: U.S.A.

ZIP: 0110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
PRING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
PRING DATE: 30-JAN-96
PRIOR APPLICATION NUMBER: 08/380,167
PRILNG DATE: 30-JAN-95
ATTONNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
REGISTRATION WUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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99.4%;
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Best Local Similarity 99.44
Matches 175, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                         Boston
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; LENGTH: 1152
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PCT-US96-01314-43
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1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC Compatible
COMPUTER: PLOPSY disk
COMPUTER: PLANCE COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/365,652
FILING DATE: 2-DEC-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 2-DEC-1994
ATPONEX/AGENT INFORMATION:
AMANDE: MAINTENER: US 08/362,652
FILING DATE: 21-DEC-1994
ATPONEX/AGENT INFORMATION:
AMANDE: MAINTENER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 2786 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                    United States
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                                                                         60606-6402
                                  Illinois
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US-08-362-652-3
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                  Sequence 3, Application US/08286889
Patent No. 5470953
CENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                        STATE: Illinois
COUNTRY: United States
ZUP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY FAGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                           Chicago
US-08-286-889-3
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27866/32797

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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
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                                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                     264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFOVNNFE 319
                                                                                                                                                                                                                                                                                                                                                 121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTON: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
  97.9%; Score 903; DB 1; Length 1153; 99.4%; Pred. No. 1e-91; Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicas.
STATE: Illinois
COUNTRY: United States
TIP: 60606-6402
Query Match 97.9
Best Local Similarity 99.4
Matches 175; Conservative
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61 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 BFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVWEQLKKSKTLFSLMQYSEEFRIHFTFK 203
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Patent No. 5831029

GENERAL INFORMATION:
GALLAINTON:
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQCNNFE 176
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Pred. No. 1e-91;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC rempatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
                                     PRILIM DATE: 23-DEC-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGRYT INFORMATION:
NAME: Williams JT., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFRENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312-474-0448
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
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                                                                                                                                                                                                                                                                                                                                       TELERAX: 312-4/1.
TELERAX: 312-4/1.
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
STANTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.43
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-482-293A-3
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Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATSHALL: O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                   27866/32391
                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,65
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                               FILING DATE:
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Query Match 97.9%;
Best Local Similarity 99.4%;
Matches 175; Conservative
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                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino aci
                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-943-363-3
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 175; Conserva
                                                                                                                                                                                                                amino acid
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US-08-943-363-3
; Sequence 3, Application US/08943363
; Sequence 3, Application US/0894363
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
; TITLE OF INFORTION: No. 5837478el Human 2 Integrin Alpha Subunit
; VADBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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                                                                                                   NAME: /williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              TELEFAX: 312-474-0448
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              LENGTH: 1153 amino acids TYPE: amino acid
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                          single
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Pred. No. 1e-91;
0; Mismatches 1; Indels
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
                                                                           27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-02-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATCHIN Ver. 2.0
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REPERENCE/DOCKET NUMBER: 27866,
TELECOMMUNICATION INFORMATION:
TELEFHONE: 312-474-6300
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; Sequence 3, Application US/09193043
; Patent No. 6251395
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264 DPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFE 319
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Galiatin, Michael W.
APPLICANT: Galiatin, Michael W.
TITLE OF INVENTION: NO. 6432404el Human Beta-2
FILE REPRENCE: 27866/36646
CURRENT ERPERENCE: 27866/36646
CURRENT PILING DATE: 2000-10-13
FRICH APPLICATION NUMBER: 09/193,043
FRICH APPLICATION NUMBER: 09/193,043
FRICH FILING DATE: 1998-11-16
FRICH FILING DATE: 1996-02-22
FRICH APPLICATION NUMBER: 08/265
FRICH APPLICATION NUMBER: 08/266,889
FRICH FILING DATE: 1994-08-05
FRICH FILING DATE: 1994-08-05
FRICH FILING DATE: 1994-12-21
FRICH FILING DATE: 1994-12-21
FRICH REPLICATION NUMBER: 08/362,652
FRICH APPLICATION NUMBER: 08/362,652
FRICH APPLICATION NUMBER: 08/362,652
FRICH APPLICATION NUMBER: 08/362,652
FRICH APPLICATION NUMBER: 08/343,363
FRICH APPLICATION NUMBER: 08/343,363
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Sequence 3, Application US/09350259
Fatent No. 6620915
GENERAL INPORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6620915el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER PELING DATE: 1998-11-16
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/36,652
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-12-21
                                                                                                                                                                                                            Sequence 3, Application US/09688307A Patent No. 6432404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, Michael W.
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Best Local Similarity 99.4
Matches 175, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-688-307A-3
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NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 99.4
Matches 175; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
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